

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
31 October 2002 (31.10.2002)

PCT

(10) International Publication Number
WO 02/086085 A2

(51) International Patent Classification⁷: C12N

(21) International Application Number: PCT/US02/12801

(22) International Filing Date: 24 April 2002 (24.04.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/285,683 24 April 2001 (24.04.2001) US

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(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR,

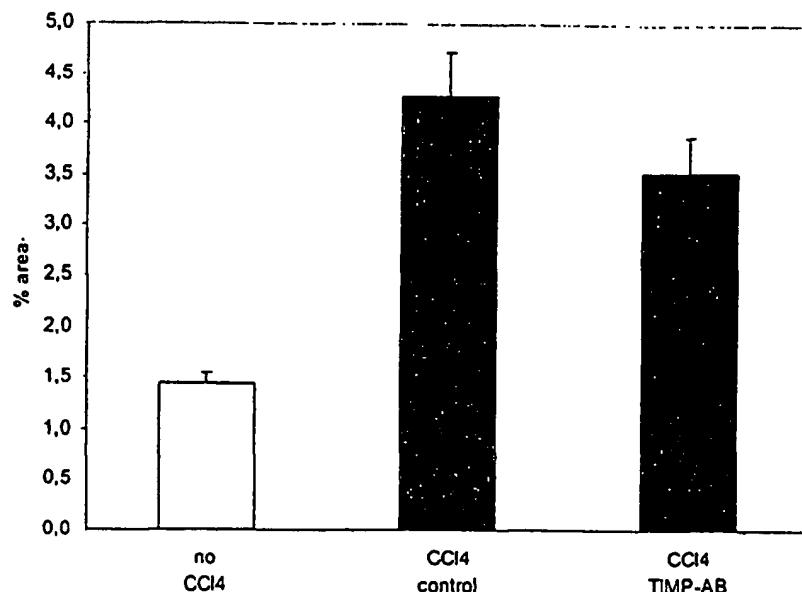
[Continued on next page]



WO 02/086085 A2

(54) Title: HUMAN TIMP-1 ANTIBODIES

Morphometry



(57) Abstract: Human antibodies that bind to TIMP-1 can be used as reagents to diagnose and treat disorders in which TIMP-1 is elevated, such as liver fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus nephritis, glomerulosclerotic renal disease, benign prostate hypertrophy, colon cancer, lung cancer, and idiopathic pulmonary fibrosis.



GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent
(BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,
NE, SN, TD, TG).

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

Published:

- *without international search report and to be republished upon receipt of that report*

HUMAN TIMP-1 ANTIBODIES

[01] This application claims priority to and incorporates by reference co-pending provisional application Serial No. 60/285,683 filed April 24, 2001.

FIELD OF THE INVENTION

[02] The invention relates to TIMP-1-binding human antibodies.

BACKGROUND OF THE INVENTION

[03] Tissue inhibitors of metalloproteases (TIMPs) inhibit metalloproteases, a family of endopeptide hydrolases. Metalloproteases are secreted by connective tissue and hematopoietic cells, use Zn^{2+} or Ca^{2+} for catalysis, and may be inactivated by metal chelators as well as TIMP molecules. Matrix metalloproteases (MMPs) participate in a variety of biologically important processes, including the degradation of many structural components of tissues, particularly the extracellular matrix (ECM).

[04] Degradation of extracellular matrix tissue is desirable in processes where destruction of existing tissues is necessary, *e.g.*, in embryo implantation (Reponen *et al.*, *Dev. Dyn.* 202, 388-96, 1995), embryogenesis, and tissue remodeling. Imbalance between synthesis and degradation of matrix proteins, however, can result in diseases such as liver fibrosis (Iredale *et al.*, *Hepatology* 24, 176-84, 1996). This imbalance can occur, for example, if levels of TIMPs are increased. Disorders in which TIMP-1 levels of increased include, for example, liver fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic pulmonary fibrosis, benign prostate hypertrophy, lung cancer, and colon cancer. *See, e.g.*, Inokubo

et al., *Am. Heart J.* 141, 211-17, 2001; Ylisirnio *et al.*, *Anticancer Res.* 20, 1311-16, 2000; Holten-Andersen *et al.*, *Clin. Cancer Res.* 6, 4292-99, 2000; Holten-Andersen *et al.*, *Br. J. Cancer* 80, 495-503, 1999; Peterson *et al.*, *Cardiovascular Res.* 46, 307-15, 2000; Arthur *et al.*, *Alcoholism: Clinical and Experimental Res.* 23, 840-43, 1999; Iredale *et al.*, *Hepatol.* 24, 176-84, 1996.

[06] There is a need in the art for reagents and methods of inhibiting TIMP-1 activity, which can be used to provide therapeutic effects.

BRIEF SUMMARY OF THE INVENTION

[07] It is an object of the present invention to provide reagents and methods of inhibiting TIMP-1 activity. This and other objects of the invention are provided by one or more of the embodiments described below.

[08] One embodiment of the invention is a purified preparation of a human antibody, wherein the antibody binds to a tissue inhibitor of metalloprotease-1 (TIMP-1) and neutralizes a matrix metalloprotease (MMP)-inhibiting activity of the TIMP-1.

[09] Another embodiment of the invention is a purified preparation of a first human antibody which comprises a VHCDR3 region comprising an amino acid sequence selected from the group consisting of SEQ ID NOS:1-43 and 360.

[10] Still another embodiment of the invention is a purified preparation of a first human antibody which comprises a VLCDR3 region comprising an amino acid sequence selected from the group consisting of SEQ ID NOS:44-86 and 365-379.

[11] Yet another embodiment of the invention is a purified preparation of a first human antibody which has TIMP-1 binding and MMP-inhibiting activity characteristics of a second human antibody. The second antibody comprises a VHCDR3 and VLCDR3 amino acid sequence pair selected from the group consisting of SEQ ID NOS:1 and 44, SEQ ID NOS:2 and 45, SEQ ID NO:3 and 46, SEQ ID NOS:4 and 47, SEQ ID NOS:5

and 48, SEQ ID NOS:6 and 49, SEQ ID NOS:7 and 50, SEQ ID NOS:3 and 44, SEQ ID NOS:3 and 45, SEQ ID NOS:3 and 47, SEQ ID NOS:3 and 48, SEQ ID NOS:3 and 49, SEQ ID NOS:3 and 50, SEQ ID NOS:7 and 44, SEQ ID NOS:7 and 45, SEQ ID NOS:7 and 47, SEQ ID NOS:7 and 48, SEQ ID NOS:8 and 51, SEQ ID NOS:9 and 52, SEQ ID NOS:10 and 53, SEQ ID NOS:11 and 54, SEQ ID NOS:12 and 55, SEQ ID NOS:13 and 56, SEQ ID NOS:14 and 57, SEQ ID NOS:15 and 58, SEQ ID NOS:16 and 59, SEQ ID NOS:17 and 60, SEQ ID NOS:18 and 61, SEQ ID NOS:19 and 62, SEQ ID NOS:20 and 63, SEQ ID NOS:21 and 64, SEQ ID NOS:22 and 65, SEQ ID NOS:23 and 66, SEQ ID NOS:24 and 67, SEQ ID NOS:25 and 68, SEQ ID NOS:26 and 69, SEQ ID NOS:27 and 70, SEQ ID NOS:28 and 71, SEQ ID NOS:29 and 72, SEQ ID NOS:30 and 73, SEQ ID NOS:31 and 74, SEQ ID NOS:32 and 75, SEQ ID NOS:33 and 76, SEQ ID NOS:34 and 77, SEQ ID NOS:35 and 78, SEQ ID NOS:36 and 79, SEQ ID NOS:37 and 80, SEQ ID NOS:38 and 81, SEQ ID NOS:39 and 82, SEQ ID NOS:40 and 83, SEQ ID NOS:41 and 84, SEQ ID NOS:42 and 85, SEQ ID NOS:43 and 86, SEQ ID NOS:3 and 48, SEQ ID NOS:360 and 48, SEQ ID NOS:3 and 365, SEQ ID NOS:16 and 59, SEQ ID NOS:18 and 61, SEQ ID NOS:34 and 77, SEQ ID NOS:34 and 379, SEQ ID NOS:18 and 376, SEQ ID NOS:18 and 377, and SEQ ID NOS:18 and 378.

[12] Even another embodiment of the invention is a purified preparation of a human antibody comprising a VHCDR3 and VLCDR3 amino acid sequence pair selected from the group consisting of SEQ ID NOS:1 and 44, SEQ ID NOS:2 and 45, SEQ ID NOS:3 and 46, SEQ ID NOS:4 and 47, SEQ ID NOS:5 and 48, SEQ ID NOS:6 and 49, SEQ ID NOS:7 and 50, SEQ ID NOS:3 and 44, SEQ ID NOS:3 and 45, SEQ ID NOS:3 and 47, SEQ ID NOS:3 and 48, SEQ ID NOS:3 and 49, SEQ ID NOS:3 and 50, SEQ ID NOS:7 and 44, SEQ ID NOS:7 and 45, SEQ ID NOS:7 and 47, SEQ ID NOS:7 and 48, SEQ ID NOS:7 and 49, SEQ ID NOS:11 and 54, SEQ ID NOS:12 and 55, SEQ ID NOS:13 and 56, SEQ ID NOS:14 and 57, SEQ ID NOS:15 and 58, SEQ ID NOS:16 and 59, SEQ ID NOS:17 and 60, SEQ ID NOS:18 and 61, SEQ ID NOS:19 and 62, SEQ ID NOS:20 and 63, SEQ ID NOS:21 and 64, SEQ ID NOS:22 and 65, SEQ ID NOS:23 and 66, SEQ ID NOS:24 and 67, SEQ ID NOS:25 and 68, SEQ

ID NOS:26 and 69, SEQ ID NOS: 27 and 70, SEQ ID NOS:28 and 71, SEQ ID NOS:29 and 72, SEQ ID NOS:30 and 73, SEQ ID NOS:31 and 74, SEQ ID NOS:32 and 75, SEQ ID NOS:33 and 76, SEQ ID NOS:34 and 77, SEQ ID NOS:35 and 78, SEQ ID NOS:36 and 79, SEQ ID NOS:37 and 80, SEQ ID NOS:38 and 81, SEQ ID NOS:39 and 82, SEQ ID NOS:40 and 83, SEQ ID NOS:41 and 84, SEQ ID NOS:42 and 85, SEQ ID NOS:43 and 86, SEQ ID NOS:3 and 48, SEQ ID NOS:360 and 48, SEQ ID NOS:3 and 365, SEQ ID NOS:16 and 59, SEQ ID NOS:18 and 61, SEQ ID NOS:34 and 77, SEQ ID NOS:34 and 379, SEQ ID NOS:18 and 376, SEQ ID NOS:18 and 377, and SEQ ID NOS:18 and 378.

[13] A further embodiment of the invention is a purified preparation of a human antibody which comprises a heavy chain and a light chain amino acid pair selected from the group consisting of SEQ ID NOS:140 and 97, SEQ ID NOS:141 and 98, SEQ ID NOS:142 and 99, SEQ ID NOS:143 and 100, SEQ ID NOS:144 and 101, SEQ ID NOS:145 and 102, SEQ ID NOS:146 and 103, SEQ ID NOS:142 and 97, SEQ ID NOS:142 and 98, SEQ ID NOS:142 and 100, SEQ ID NOS:142 and 101, SEQ ID NOS:142 and 102, SEQ ID NOS:142 and 103, SEQ ID NOS:146 and 97, SEQ ID NOS:146 and 98, SEQ ID NOS:146 and 100, SEQ ID NOS:146 and 101, SEQ ID NOS:148 and 104, SEQ ID NOS:148 and 105, SEQ ID NOS:149 and 106, SEQ ID NOS:150 and 107, SEQ ID NOS:151 and 108, SEQ ID NOS:152 and 109, SEQ ID NOS:153 and 110, SEQ ID NOS:154 and 111, SEQ ID NOS:155 and 112, SEQ ID NOS:156 and 113, SEQ ID NOS:157 and 114, SEQ ID NOS:158 and 115, SEQ ID NOS:159 and 116, SEQ ID NOS:160 and 117, SEQ ID NOS:161 and 118, SEQ ID NOS:162 and 119, SEQ ID NOS:163 and 120, SEQ ID NOS:164 and 121, SEQ ID NOS:165 and 122, SEQ ID NOS:166 and 123, SEQ ID NOS:167 and 124, SEQ ID NOS:168 and 125, SEQ ID NOS:169 and 126, SEQ ID NOS:170 and 127, SEQ ID NOS:171 and 128, SEQ ID NOS:172 and 129, SEQ ID NOS:173 and 130, SEQ ID NOS:174 and 131, SEQ ID NOS:175 and 132, SEQ ID NOS:176 and 133, SEQ ID NOS:177 and 134, SEQ ID NOS:178 and 135, SEQ ID NOS:179 and 136, SEQ ID NOS:180 and 137, SEQ ID NOS:181 and 138, and SEQ ID NOS:182 and 139.

- [14] Another embodiment of the invention is a pharmaceutical composition comprising a human antibody and a pharmaceutically acceptable carrier. The human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1.
- [15] Yet another embodiment of the invention is a purified polynucleotide which encodes a human antibody comprising a VHCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:1-43 and 360. The human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1.
- [16] Even another embodiment of the invention is a purified polynucleotide which encodes a human antibody comprising a VLCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:44-86 and 365-379. The human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1.
- [17] Still another embodiment of the invention is an expression vector comprising a polynucleotide which encodes a human antibody comprising a VHCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:1-43 and 360. The human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1.
- [18] A further embodiment of the invention is an expression vector comprising a polynucleotide which encodes a human antibody comprising a VHCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:1-43 and 360. The human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1. The VHCDR3 region is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:227-269.
- [19] Another embodiment of the invention is an expression vector comprising a polynucleotide which encodes a human antibody comprising a VLCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID

NOS:44-86 and 365-379. The human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1.

- [20] Yet another embodiment of the invention is an expression vector comprising a polynucleotide which encodes a human antibody comprising a VLCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:44-86 and 365-379. The human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1. The VLCDR3 region is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:184-226.
- [21] Still another embodiment of the invention is an expression vector comprising a polynucleotide which encodes a human antibody comprising a VHCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:1-43 and 360. The human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1. The human antibody comprises a heavy chain having an amino acid sequence selected from the group consisting of SEQ ID NOS:140-182.
- [22] Even another embodiment of the invention is an expression vector comprising a polynucleotide which encodes a human antibody comprising a VHCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:1-43 and 360. The human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1. The human antibody comprises a heavy chain having an amino acid sequence selected from the group consisting of SEQ ID NOS:140-182. The heavy chain is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:269-311.
- [23] A further embodiment of the invention is an expression vector comprising a polynucleotide which encodes a human antibody comprising a VLCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:44-86 and 365-379. The human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1. The human antibody comprises a light chain

having an amino acid sequence selected from the group consisting of SEQ ID NOS:97-139.

- [24] Another embodiment of the invention is an expression vector comprising a polynucleotide which encodes a human antibody comprising a VLCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:44-86 and 365-379. The human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1. The human antibody comprises a light chain having an amino acid sequence selected from the group consisting of SEQ ID NOS:97-139. The light chain is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:312-354.
- [25] Yet another embodiment of the invention is a host cell comprising an expression vector. The expression vector comprises a polynucleotide which encodes a human antibody comprising a VHCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:1-43 and 360, wherein the human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1.
- [26] Yet another embodiment of the invention is a host cell comprising an expression vector. The expression vector comprises a polynucleotide which encodes a human antibody comprising a VHCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:1-43 and 360, wherein the human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1. The VHCDR3 region is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:227-269.
- [27] Still another embodiment of the invention is a host cell comprising an expression vector. The expression vector comprises a polynucleotide which encodes a human antibody comprising a VLCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:44-86 and 365-379. The human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1.

[28] A further embodiment of the invention is a host cell comprising an expression vector. The expression vector comprises a polynucleotide which encodes a human antibody comprising a VLCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:44-86 and 365-379. The human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1. The VLCDR3 region is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:184-226.

[29] Another embodiment of the invention is a host cell comprising an expression vector. The expression vector comprises a polynucleotide which encodes a human antibody comprising a VHCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:1-43 and 360, wherein the human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1. The human antibody comprises a heavy chain having an amino acid sequence selected from the group consisting of SEQ ID NOS:140-182.

[30] Still another embodiment of the invention is a host cell comprising an expression vector. The expression vector comprises a polynucleotide which encodes a human antibody comprising a VHCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:1-43 and 360, wherein the human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1. The human antibody comprises a heavy chain having an amino acid sequence selected from the group consisting of SEQ ID NOS:140-182. The heavy chain is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:269-311.

[31] Yet another embodiment of the invention is a host cell comprising an expression vector. The expression vector comprises a polynucleotide which encodes a human antibody comprising a VLCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:44-86 and 365-379. The human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1. The human

antibody comprises a light chain having an amino acid sequence selected from the group consisting of SEQ ID NOS:97-139.

- [32] Even another embodiment of the invention is a host cell comprising an expression vector. The expression vector comprises a polynucleotide which encodes a human antibody comprising a VLCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:44-86 and 365-379. The human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1. The human antibody comprises a light chain having an amino acid sequence selected from the group consisting of SEQ ID NOS:97-139. The light chain is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:312-354.
- [33] A further embodiment of the invention is a method of making a human antibody. The host cell of claim 43 is cultured under conditions whereby the antibody is expressed. The human antibody is purified from the host cell culture.
- [34] Another embodiment of the invention is a method of decreasing an MMP-inhibiting activity of a TIMP-1. The TIMP-1 is contacted with a human antibody that binds to the TIMP-1. The MMP-inhibiting activity of the TIMP-1 is decreased relative to MMP-inhibiting activity of the TIMP-1 in the absence of the antibody.
- [35] Still another embodiment of the invention is a method of ameliorating symptoms of a disorder in which TIMP-1 is elevated. An effective amount of a human antibody which neutralizes an MMP-inhibiting activity of the TIMP-1 is administered to a patient having the disorder. Symptoms of the disorder are thereby ameliorated.
- [36] A further embodiment of the invention is a method of detecting a TIMP-1 in a test preparation. The test preparation is contacted with a human antibody that specifically binds to the TIMP-1. The test preparation is assayed for the presence of an antibody-TIMP-1 complex.

[37] Even another embodiment of the invention is a method to aid in diagnosing a disorder in which a TIMP-1 level is elevated. A sample from a patient suspected of having the disorder is contacted with a human antibody that binds to TIMP-1. The sample is assayed for the presence of an antibody-TIMP-1 complex. Detection of an amount of the complex which is greater than an amount of the complex in a normal sample identifies the patient as likely to have the disorder.

[38] The invention thus provides human antibodies which bind to TIMP-1 and neutralize MMP-inhibiting activity of TIMP-1. These antibodies can be used, *inter alia*, in diagnostic and therapeutic methods.

BRIEF DESCRIPTION OF THE FIGURES

[39] FIG. 1. Protein sequences encoded by the HuCAL® V_H and V_L Fab master genes. Seven V_H and V_L sequences are aligned, and the approximate location of restriction endonuclease sites introduced into the corresponding DNA sequences are indicated. The numbering is according to VBASE except for the gap in Vl position 9. In VBASE the gap is set at position 10. See also Chothia *et al.* (1992) *J. Mol. Biol.* 227, 776-798, Tomlinson *et al.* (1995) *EMBO J.* 14, 4628-4638 and Williams *et al.* (1996) *J. Mol. Biol.* 264, 220-232).

[40] FIG. 2. Nucleotide sequences of the HuCAL® V_H and V_L Fab master genes.

[41] FIG. 3. Fab display vector pMORPH® 18 Fab 1.

[42] FIG. 4. Vector map of pMORPH® x9Fab1_FS.

[43] FIG. 5. Sequence comparison between human and rat TIMP-1. Sequence regions in bold were used for peptide synthesis. Residues that make stronger direct contacts with MMP-3 are italicized, and residues that make weaker direct contacts with MMP-3 are underlined (Gomis-Ruth *et al.*, 1997).

Methods of decreasing MMP-inhibiting activity of human TIMP-1

- [88] The invention provides methods of decreasing an MMP-inhibiting activity of human or rat TIMP-1. Such methods can be used therapeutically, as described below, or in a research setting. Thus, the methods can be carried out in a cell-free system, in a cell culture system, or *in vivo*. *In vivo* methods of decreasing MMP-inhibiting activity of human or rat TIMP-1 are described below.
- [89] Human TIMP-1 is contacted with a human antibody that binds to the human TIMP-1, thereby decreasing the MMP-inhibiting activity of the human TIMP-1 relative to human TIMP-1 activity in the absence of the antibody. The antibody can be added directly to the cell-free system, cell culture system, or to an animal subject or patient, or can be provided by means of an expression vector encoding the antibody.

Diagnostic methods

- [90] The invention also provides diagnostic methods, with which human or rat TIMP-1 can be detected in a test preparation, including without limitation a sample of serum, lung, liver, heart, kidney, colon, a cell culture system, or a cell-free system (e.g., a tissue homogenate). Such diagnostic methods can be used, for example, to diagnose disorders in which TIMP-1 is elevated. Such disorders include, but are not limited to, liver fibrosis, alcoholic liver disease, cardiac fibrosis, acute cardiac syndrome, lupus nephritis, glomerulosclerotic renal disease, benign prostate hypertrophy, lung cancer, colon cancer, and idiopathic pulmonary fibrosis. When used for diagnosis, detection of an amount of the antibody-TIMP-1 complex in a test sample from a patient which is greater than an amount of the complex in a normal sample identifies the patient as likely to have the disorder.
- [91] The test preparation is contacted with a human antibody of the invention, and the test preparation is then assayed for the presence of an antibody-TIMP-1 complex. If desired, the human antibody can comprise a detectable label, such as a fluorescent, radioisotopic,

chemiluminescent, or enzymatic label, such as horseradish peroxidase, alkaline phosphatase, or luciferase.

[92] Optionally, the antibody can be bound to a solid support, which can accommodate automation of the assay. Suitable solid supports include, but are not limited to, glass or plastic slides, tissue culture plates, microtiter wells, tubes, silicon chips, or particles such as beads (including, but not limited to, latex, polystyrene, or glass beads). Any method known in the art can be used to attach the antibody to the solid support, including use of covalent and non-covalent linkages, passive absorption, or pairs of binding moieties attached to the antibody and the solid support. Binding of TIMP-1 and the antibody can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and microcentrifuge tubes.

Therapeutic methods

[93] The invention also provides methods of ameliorating symptoms of a disorder in which TIMP-1 is elevated. These disorders include, without limitation, liver fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic pulmonary fibrosis, benign prostate hypertrophy, lung cancer, colon cancer, and scarring. See, e.g., Inokubo *et al.*, *Am. Heart J.* 141, 211-17, 2001; Ylisimio *et al.*, *Anticancer Res.* 20, 1311-16, 2000; Holten-Andersen *et al.*, *Clin. Cancer Res.* 6, 4292-99, 2000; Holten-Andersen *et al.*, *Br. J. Cancer* 80, 495-503, 1999; Peterson *et al.*, *Cardiovascular Res.* 46, 307-15, 2000; Arthur *et al.*, *Alcoholism: Clinical and Experimental Res.* 23, 840-43, 1999; Iredale *et al.*, *Hepatol.* 24, 176-84, 1996.

[94] Human antibodies of the invention are particularly useful for treating liver fibrosis. All chronic liver diseases cause the development of fibrosis in the liver. Fibrosis is a programmed uniform wound healing response. Toxic damage or injury caused by foreign proteins cause the deposition of extracellular matrix such as collagen, fibronectin, and laminin. Liver fibrosis and cirrhosis can be caused by chronic degenerative diseases

of the liver such as viral hepatitis, alcohol hepatitis, autoimmune hepatitis, primary biliary cirrhosis, cystic fibrosis, hemochromatosis, Wilson's disease, and non-alcoholic steato-hepatitis, as well as chemical damage.

[95] Altered degradation and synthesis of extracellular matrix (particularly collagens) play central roles in pathogenesis of liver fibrosis. In the early phases, hepatic stellate cells (HSC) are initially activated and release matrix metalloproteases with the ability to degrade the normal liver matrix. When HSC are fully activated, there is a net down-regulation of matrix degradation mediated by increased synthesis and extracellular release of tissue inhibitors of metalloprotease (TIMP)-1 and -2. The dynamic regulation of activity of metalloproteases during liver fibrosis makes them and their inhibitors targets for therapeutic intervention.

[96] Human antibodies of the invention are also particularly useful for treating lung fibrosis. Lung airway fibrosis is a hallmark of airway remodeling in patients with chronic asthma, so human antibodies of the invention are also particularly useful for chronic asthma. Airway remodeling is a well-recognized feature in patients with chronic asthma. TIMP-1 but not TIMP-2 levels were significantly higher in untreated asthmatic subjects than in glucocorticoid-treated subjects or controls ($p < 0.0001$), and were far greater than those of MMP-1, MMP-2, MMP-3, and MMP-9 combined (Mautino *et al.*, Am J Respir Crit Care Med 1999 160:324-330). TIMP-1 mRNA and protein expression are selectively and markedly increased in a murine model of bleomycin-induced pulmonary fibrosis (Am. J. Respir. Cell Mol. Bio. 24:599-607, 2001). This specific elevation of TIMP-1 without increase in MMPs in asthma patients suggests that inhibition of TIMP-1 by an antibody can restore normal collagen degradation in the lung.

[97] Human antibodies of the invention are also particularly useful for treating cancer. TIMP-1 protein has been found to be elevated in plasma of colon (Holten-Andersen *et al.*, Br J Cancer 1999, 80:495-503) and prostate (Jung *et al.*, Int J Cancer, 1997, 74:220-223) cancer patients, and high TIMP-1 plasma level correlates with poor clinical outcome of

colon cancer (Holten-Andersen et al., *Clin Cancer Res* 2000 6:4292-4299). TIMP-1 induces dose-dependent proliferation of breast tumorigenic clonal cell line and tyrosine phosphorylation (Luparello et al., *Breast Cancer Res Treat*, 1999, 54:235-244). Therefore, the use of antibody against TIMP-1 may block its ability to induce cancer.

[98] Human TIMP-1 antibodies can be used to prevent or diminish scar formation, such as scar formation after surgery (particularly ophthalmic surgery) or injury (such as a burn, scrape, crush, cut or tear injury).

[99] In one embodiment of the invention, a therapeutically effective dose of a human antibody of the invention is administered to a patient having a disorder in which TIMP-1 is elevated, such as those disorders described above. Symptoms of the disorder, including deposition of extracellular matrix, as well as loss of tissue or organ function, are thereby ameliorated.

Determination of a Therapeutically Effective Dose

[100] The determination of a therapeutically effective dose is well within the capability of those skilled in the art. A therapeutically effective dose refers to that amount of human antibody that reduces MMP-inhibiting activity of the TIMP-1 relative to the activity which occurs in the absence of the therapeutically effective dose.

[101] The therapeutically effective dose can be estimated initially either in cell culture assays or in animal models, usually rats, mice, rabbits, dogs, or pigs. The animal model also can be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans. A rat liver fibrosis model is described in Example 6.

[102] Therapeutic efficacy and toxicity, e.g., ED₅₀ (the dose therapeutically effective in 50% of the population) and LD₅₀ (the dose lethal to 50% of the population) of a human antibody, can be determined by standard pharmaceutical procedures in cell cultures or experimental

animals. The dose ratio of toxic to therapeutic effects is the therapeutic index, and it can be expressed as the ratio, LD₅₀/ED₅₀.

[103] Pharmaceutical compositions that exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies is used in formulating a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, sensitivity of the patient, and the route of administration.

[104] The exact dosage will be determined by the practitioner, in light of factors related to the patient who requires treatment. Dosage and administration are adjusted to provide sufficient levels of the human antibody or to maintain the desired effect. Factors that can be taken into account include the severity of the disease state, general health of the subject, age, weight, and gender of the subject, diet, time and frequency of administration, drug combination(s), reaction sensitivities, and tolerance/response to therapy. Long-acting pharmaceutical compositions can be administered every 3 to 4 days, every week, or once every two weeks depending on the half-life and clearance rate of the particular formulation.

[105] Polynucleotides encoding human antibodies of the invention can be constructed and introduced into a cell either *ex vivo* or *in vivo* using well-established techniques including, but not limited to, transferrin-polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated cellular fusion, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, "gene gun," and DEAE- or calcium phosphate-mediated transfection.

[106] Effective *in vivo* dosages of an antibody are in the range of about 5 mg to about 50 mg/kg, about 50 mg to about 5 mg/kg, about 100 mg to about 500 mg/kg of patient body weight, and about 200 to about 250 mg/kg of patient body weight. For administration of polynucleotides encoding the antibodies, effective *in vivo* dosages are in the range of

about 100 ng to about 200 ng, 500 ng to about 50 mg, about 1 mg to about 2 mg, about 5 mg to about 500 mg, and about 20 mg to about 100 mg of DNA.

[107] The mode of administration of human antibody-containing pharmaceutical compositions of the invention can be any suitable route which delivers the antibody to the host. Pharmaceutical compositions of the invention are particularly useful for parenteral administration, *i.e.*, subcutaneous, intramuscular, intravenous, or intranasal administration.

[108] All patents, patent applications, and references cited in this disclosure are expressly incorporated herein by reference. The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific examples, which are provided for purposes of illustration only and are not intended to limit the scope of the invention.

EXAMPLE 1

Construction of a Human Combinatorial Antibody Library (HuCAL® Fab 1)

[109] *Cloning of HuCAL® Fab 1.* HuCAL® Fab 1 is a fully synthetic, modular human antibody library in the Fab antibody fragment format. HuCAL® Fab 1 was assembled starting from an antibody library in the single-chain format (HuCAL® -scFv, Knappik *et al.*, *J. Mol. Biol.* 296, 55, 2000). HuCAL® Fab 1 was cloned into a phagemid expression vector pMORPH® 18 Fab1 (FIG. 3). This vector comprises the Fab fragment with a phoA signal sequence fused at the C-terminus to a truncated gene III protein of filamentous phage, and further comprises the light chain VL-CL with an ompA signal sequence. Both chains are under the control of the lac operon. The constant domains C7, C7, and CH are synthetic genes fully compatible with the modular system of HuCAL® (Knappik *et al.*, 2000).

[110] First, the V7 and V7 libraries were isolated from HuCAL® -scFv. V71 fragments were amplified by 15 PCR cycles (Pwo polymerase) with primers 5'-

GTGGGGTTCCGATATTC-3' (SEQ ID NO:380) and 5'-AGCGTCACA-CTCGGTGGCTTCGGCTGGCTGCGTA-3' (SEQ ID NO:381). PCR-products were digested with EcoRV / DralII and gel-purified. VL γ -chains were obtained by restriction digest with EcoRV / BstWI and gel-purified. These V γ and V γ libraries were cloned into pMORPH[®] 18 Fab1 cut with EcoRV / DralII and EcoRV / BstWI, respectively. After ligation and transformation in *E. coli* TG-1, library sizes of 4.14×10^8 and 1.6×10^8 , respectively, were obtained, in both cases exceeding the V γ diversity of HuCAL[®]-scFv.

[111] Similarly, the VH library was isolated from HuCAL[®]-scFv by restriction digest using *Sph*I / *Mun*I. This VH library was cloned into the pMORPH[®] 18-V γ and V γ libraries cut with *Sph*I / *Mun*I. After ligation and transformation in *E. coli* TG-1, a total library size of 2.09×10^9 was obtained, with 67% correct clones (as identified by sequencing of 207 clones).

[112] *Phagemid rescue, phage amplification and purification.* HuCAL[®] Fab was amplified in 2 x TY medium containing 34 μ g/ml chloramphenicol and 1 % glucose (2 x TY-CC). After helper phage infection (VCSM13) at 37°C at an OD₆₀₀ of about 0.5, centrifugation and resuspension in 2 x TY / 34 μ g/ml chloramphenicol/ 50 μ g/ml kanamycin, cells were grown overnight at 30°C. Phage were PEG-precipitated from the supernatant (Ausubel *et al.*, 1998), resuspended in PBS/20% glycerol, and stored at -80°C. Phage amplification between two panning rounds was conducted as follows: mid-log phase TG1-cells were infected with eluted phage and plated onto LB-agar supplemented with 1% of glucose and 34 μ g/ml of chloramphenicol. After overnight incubation at 30°C, colonies were scraped off and adjusted to an OD₆₀₀ of 0.5. Helper phage were added as described above.

EXAMPLE 2***Solid phase panning***

[113] Wells of MaxiSorp™ microtiter plates (Nunc) were coated with rat- or human TIMP protein diluted to 50 µg/ml dissolved in PBS (2 µg/well). After blocking with 5% non-fat dried milk in PBS, 1–5 × 10¹² HuCAL® Fab phage purified as above were added for 1 h at 20°C. After several washing steps, bound phage were eluted by pH-elution with 100 mM triethylamine and subsequent neutralization with 1M TRIS-Cl pH 7.0. See Krebs *et al.*, *J. Immunol. Meth.* 254, 67, 2001. Two to three rounds of panning were performed with phage amplification conducted between each round as described above.

EXAMPLE 3***Solution panning***

[114] Biotinylated antigen was diluted to 40 nM in PBS, 1013 HuCAL®-Fab 1 phage were added and incubated for 1 h at 20°C. Phage-antigen complexes were captured on Neutravidin plates (Pierce). After several washing steps, bound phages were eluted by different methods (Krebs *et al.*, 2001). Two rounds of panning were routinely performed.

EXAMPLE 4***Subcloning of selected Fab fragments for expression***

[115] The Fab-encoding inserts of the selected HuCAL® Fab 1 fragments were subcloned into the expression vector pMORPH® x7_FS (Knappik *et al.*, *J. Mol. Biol.* 296, 55, 2000) to facilitate rapid expression of soluble Fab. The DNA preparation of the selected HuCAL® Fab 1 clones was digested with *Xba*I / *Eco*RI, thus cutting out the Fab encoding insert (*ompA-VL* and *phoA-Fc*). Subcloning of the purified inserts into the *Xba*I / *Eco*RI cut vector pMORPH® x7, previously carrying a scFv insert, produces a Fab expression vector designated pMORPH® x9_Fab1_FS (FIG. 4). Fabs expressed in this vector carry two C-terminal tags (FLAG™ and Strep-tagII) for detection and purification.

EXAMPLE 5*Identification of TIMP-binding Fab fragments by ELISA*

[116] The wells of 384-well Maxisorp ELISA plates were coated with 20 μ l/well solutions of rat TIMP or human TIMP at a concentration of 5 μ g/ml diluted in coating buffer. Expression of individual Fab in *E. coli* TG-1 from expression vector pMORPH[®] x9_FS was induced with 0.5 mM IPTG for 12 h at 30°C. Soluble Fab was extracted from the periplasm by osmotic shock (Ausubel *et al.*, 1998) and used in an ELISA. The Fab fragment was detected after incubation with alkaline phosphatase-conjugated anti-Fab antibody (Dianova), followed by development with Attophos substrate (Roche) and measurement at Ex450 nm / Em535 nm. Values at 370 nm were read out after addition of horseradish peroxidase-conjugated anti-mouse IgG antibody and POD soluble substrate (Roche Diagnostics).

EXAMPLE 6*Expression and purification of HuCAL[®] Fab I antibodies in E. coli*

[117] Expression of Fab fragments encoded by pMORPH[®] x9_FS in TG-1 cells was carried out in shaker flask cultures with 1 liter of 2xTY medium supplemented with 34 μ g/ml chloramphenicol. After induction with 0.5 mM IPTG, cells were grown at 22°C for 16 h. Periplasmic extracts of cell pellets were prepared, and Fab fragments were isolated by Strep-tactin[®] chromatography (IBA, Goettingen, Germany). The apparent molecular weights were determined by size exclusion chromatography (SEC) with calibration standards. Concentrations were determined by UV-spectrophotometry.

EXAMPLE 7*Construction of HuCAL[®] immunoglobulin expression vectors*

[118] *Heavy chain cloning.* The multiple cloning site of pcDNA3.1+ (Invitrogen) was removed (*Nhe*I / *Apa*I), and a stuffer compatible with the restriction sites used for HuCAL[®] design

was inserted for the ligation of the leader sequences (*NheI* / *EcoRI*), VH-domains (*EcoRI* / *BpuI*), and the immunoglobulin constant regions (*BpuI* / *Apal*). The leader sequence (EMBL M83133) was equipped with a Kozak sequence (Kozak, 1987). The constant regions of human IgG₁ (PIR J00228), IgG₄ (EMBL K01316), and serum IgA₁ (EMBL J00220) were dissected into overlapping oligonucleotides with lengths of about 70 bases. Silent mutations were introduced to remove restriction sites non-compatible with the HuCAL® design. The oligonucleotides were spliced by overlap extension-PCR.

[119] **Light chain cloning.** The multiple cloning site of pcDNA3.1/Zeo+ (Invitrogen) was replaced by two different stuffers. The 7-stuffer provided restriction sites for insertion of a 7-leader (*NheI* / *EcoRV*), HuCAL®-scFv V7-domains (*EcoRV* / *BsrWI*), and the 7-chain constant region (*BsrWI* / *Apal*). The corresponding restriction sites in the 7-stuffer were *NheI* / *EcoRV* (7-leader), *EcoRV* / *HpaI* (V7-domains), and *HpaI* / *Apal* (7-chain constant region). The 7-leader (EMBL Z00022) as well as the 7-leader (EMBL L27692) were both equipped with Kozak sequences. The constant regions of the human 7- (EMBL J00241) and 7-chain (EMBL M18645) were assembled by overlap extension-PCR as described above.

[120] **Generation of IgG-expressing CHO-cells.** CHO-K1 cells were co-transfected with an equimolar mixture of IgG heavy and light chain expression vectors. Double-resistant transfectants were selected with 600 µg/ml G418 and 300 µg/ml Zeocin (Invitrogen) followed by limiting dilution. The supernatant of single clones was assessed for IgG expression by capture-ELISA (see below). Positive clones were expanded in RPMI-1640 medium supplemented with 10% ultra-low IgG-FCS (Life Technologies). After adjusting the pH of the supernatant to 8.0 and sterile filtration, the solution was subjected to standard protein A column chromatography (Poros 20 A, PE Biosystems).

EXAMPLE 8

Design of the CDR3 libraries

[121] *V7 positions 1 and 2.* The original HuCAL® master genes were constructed with their authentic N-termini: V711: QS (CAGAGC), V712: QS (CAGAGC), and V713: SY (AGCTAT). Sequences containing these amino acids are shown in WO 97/08320. During HuCAL® library construction, the first two amino acids were changed to D1 to facilitate library cloning (*Eco*R1 site). All HuCAL® libraries contain V71 genes with the EcoRV site GATATC (D1) at the 5'-end. All HuCAL® kappa genes (master genes and all genes in the library) contain D1 at the 5'-end.

[122] *VH position 1.* The original HuCAL® master genes were constructed with their authentic N-termini: VH1A, VH1B, VH2, VH4, and VH6 with Q (=CAG) as the first amino acid and VH3 and VH5 with E (=GAA) as the first amino acid. Sequences containing these amino acids are shown in WO 97/08320. In the HuCAL® Fab 1 library, all VH chains contain Q (=CAG) at the first position.

[123] *V71/V73 position 85.* Because of the cassette mutagenesis procedure used to introduce the CDR3 library (Knappik *et al.*, *J. Mol. Biol.* 296, 57-86, 2000), position 85 of V71 and V73 can be either T or V. Thus, during HuCAL® scFv 1 library construction, position 85 of V71 and V73 was varied as follows: V71 original, 85T (codon ACC); V71 library, 85T or 85V (TRIM codons ACT or GTT); V73 original, 85V (codon GTC); V73 library, 85T or 85V (TRIM codons ACT or GTT); the same applies to HuCAL® Fab1.

[124] *CDR3 design.* All CDR3 residues which were kept constant are indicated in FIG. 1.

[125] *CDR3 length.* The designed CDR3 length distribution is as follows. Residues which were varied are shown in brackets (x) in FIG. 1. V kappa CDR3, 8 amino acid residues (position 89 to 96) (occasionally 7 residues), with Q90 fixed; V lambda CDR3, 8 to 10 amino acid residues (position 89 to 96) (occasionally 7-10 residues), with Q89, S90, and

D92 fixed; and VH CDR3, 5 to 28 amino acid residues (position 95 to 102) (occasionally 4-28), with D101 fixed.

EXAMPLE 9

Chronic carbon tetrachloride-induced liver fibrosis

[126] Sprague Dawley rats (200-220 g) are used in an *in vivo* model of liver fibrosis. To maximally induce microsomal metabolism of carbon tetrachloride metabolism, animals receive 1 g/l isoniazid with their drinking water starting one week before the administration of carbon tetrachloride. Carbon tetrachloride (1:1 in mineral oil) is administered orally every fifth day at a dose of 0.2 ml/100 g body weight. A human TIMP-1 antibody is administered intravenously, either once or repeatedly, during the period of carbon tetrachloride treatment. Necropsy is performed after 5-7 weeks of treatment. McLean *et al.*, *Br. J. Exp. Pathol.* 50, 502-06, 1969.

[127] Transverse cylinders of liver tissue are cut from the right liver lobe, fixed in formaldehyde, and embedded in paraffin. The amount of fibrosis in the liver is indicated by the picrosirius red-stained fibrotic areas. Picrosirius-positive areas are determined in several centrilobular fields in each section. Parameters of color detection are standardized and kept constant throughout the experiment. The field are selected using a standardized grid which covers an area of 31 mm². A Leica Quantimet 500 MC system is used for morphometry.

EXAMPLE 10

Hydroxyproline determination

[128] The method of Prockop & Udenfried, *Anal. Biochem.* 1, 228-39, 1960, can be used to determine hydroxyproline in liver tissues, with the following modifications. Liver specimens of 60-90 mg wet weight are dried and hydrolyzed in 6 N HCl at 100 °C for 17 h. The hydrolyzed material is dried and reconstituted in 5 ml of deionized water. Two

hundred microliters of this hydrolysate are mixed with 200 ml of ethanol and 200 ml chloramin T solution (0.7 % in citrate buffer [5.7 g sodium acetate, 3.75 g trisodium citrate, 0.55 g citric acid, 38.5 ml ethanol, made up to 100 ml with water]) and allowed to oxidize for 20 min at room temperature. Four hundred microliters of Ehrlich's reagent (12 g p-dimethylaminobenzaldehyde in 40 ml ethanol and 2.7 ml H₂SO₄) are added. After incubation for 3 h at 35 °C, absorbance at 573 nm is measured.

EXAMPLE 11*Affinity determination by surface plasmon resonance measurements (BIAcore™)*

[129] For affinity determination, monomeric fractions of affinity and SEC purified Fab fragments or purified IgG1 molecules were used. All experiments were conducted in HBS buffer at a flow rate of 20 μ l/min at 25°C on a BIAcore™ instrument. Antigens in 100 mM sodium acetate pH 5.0 were coupled to a CM 5 sensor chip using standard EDC-NHS coupling chemistry. Applying 3-4 μ l of 5 μ g/ml TIMP-1 typically resulted in 500 resonance units for kinetic measurements. All sensograms were fitted globally using BIA evaluation software. For monovalent Fab fragments a monovalent fit (Langmuir binding) and for IgGs a bivalent fit was applied.

EXAMPLE 12*IC₅₀ determination in human TIMP-1/human MMP-1 and rat TIMP-1/rat MMP-13 assay*

[130] Purified Fab fragments or IgGs were used for IC₅₀ determination. Antibodies were diluted in triplicate to the indicated concentrations in assay buffer containing 0.05% BSA. After addition of TIMP (final conc. 1.2 nM or 0.4 nM for modified in human TIMP-1/human MMP-1 assay), MMP (final conc. 1.2 nM or 0.4 nM for modified in human TIMP-1/human MMP-1 assay), and peptide substrate (final conc. 50 μ M) and incubation for 1-3 h at 37°C, fluorescence at Ex320 nm/Emit330 nm was measured.

[131] The following controls were included in the assay and used as reference values for IC_{50} determination:

A: MMP + substrate: this value was defined as 100% MMP activity in absence of antibody and TIMP.

B: MMP + TIMP + substrate: this value was defined as maximum inhibition achieved in the assay and calculated as a % of total MMP activity.

[132] To define the concentration of antibody that resulted in 50% reversal of inhibition (IC_{50}), the following procedure was used:

- The value for 50% reversal of inhibition (expressed as % activity MMP) was calculated as: $Y = [(A - B)/2] + B$.
- MMP activity was plotted against concentration of antibody in the assay.
- The concentration of antibody that results in 50% reversal of inhibition (Y) was read on the x-axis and defined as IC_{50} .
- Error bars in the graphs were derived from triplicate wells in one assay.
- Standard deviations for IC_{50} values were calculated from 3 independent assays.

EXAMPLE 13

Affinity maturation of selected Fab by stepwise exchange of CDR cassettes

[133] To increase affinity and biological activity of selected antibody fragments, CDR regions were optimized by cassette mutagenesis using trimucleotide directed mutagenesis (Vimekäs *et al.*, 1994). Fab fragments in expression vector pMORPH®_x9 were cloned into phagemid vector pMORPH®_18 using *Eco*RI / *Xba*I restriction sites. CDR cassettes containing several diversified positions were synthesized and cloned into Fab fragments in pMORPH®_18 using unique restriction sites (Knappik *et al.*, 2000). Affinity

maturity libraries were generated by transformation into *E. coli* TOP10F, and phage were prepared as described above. Phage displaying Fab fragments with improved affinity were selected by 2-3 rounds solution panning using stringent washing conditions (e.g., competition with 1 μ M non-biotinylated antigen or washing for up to 48 h with frequent buffer exchange) and limited amounts of antigen (0.04 – 4 nM). Seventeen human TIMP-1 antibodies were tested for affinity to human TIMP-1 (with some tested for affinity to rat TIMP-1) using a BIAcore TM assay. The K_d of these antibodies for human TIMP-1 and rat TIMP-1 are shown in Table 1.

Table 1. Overview of species cross-reactive Fab

Fab	Monovalent K_D human TIMP-1	Monovalent K_D rat TIMP-1	IC_{50} in human protease assay	IC_{50} in rat protease assay
MS-BW-25	25 +/- 16 nM*	4517 +/- 2400 nM	115 +/- 15 nM	> 300 nM
MS-BW-27	~74 nM	~ 3200 nM		Non blocking
MS-BW-21	520 +/- 20 nM	36 +/- 2 nM	> 300 nM	67 +/- 5 nM
MS-BW-38	~3 nM	~353 nM	~11 nM	> 300 nM
MS-BW-39	~7500 nM	~108 nM	> 100 nM	> 100 nM

* In cases where standard deviations are given, three independent measurements were done with Fab from three different protein expressions/purifications.

~ Indicates preliminary data, in cases where measurement was done only once.

EXAMPLE 14

Screening for Fab with improved off-rates by koff ranking using surface plasmon resonance

[134] Phage eluted after solution panning were used to infect *E. coli* TG-1 and plated on agar plates containing 34 µg/ml chloramphenicol. Clones were picked into 96 well plates and used to produce Fab fragments. On the same plate, parental clones were inoculated as controls. Soluble Fab was extracted from the periplasm by osmotic shock (Ausubel *et al.*, 1998) and used for koff ranking in BIAcore™.

[135] All measurements were conducted in HBS buffer at a flow rate of 20 µl/min at 25°C on a BIAcore™ instrument. Antigens in 100 mM sodium acetate pH 4.5 were coupled to a CM 5 sensor chip using standard EDC-NHS coupling chemistry. Applying 10 µl of 25 µg/ml TIMP-1 typically resulted in 5000 resonance units for koff ranking. All sensograms were fitted using BIA evaluation software. Clones with improved off rate were selected by comparison to parental clones.

EXAMPLE 15

Generation of species cross-reactive antibodies

[136] To maximize the likelihood of obtaining blocking antibodies that are cross-reactive between human and rat TIMP-1, alternating pannings were carried out on rat and human protein. Additionally, all antibodies selected by pannings on solely the human or rat TIMP-1 protein were analyzed for cross-reactivity in order to check for cross-reactive antibodies that might be selected by chance. Antibodies selected from these pannings were analyzed for cross-reactivity in ELISA using crude *E. coli* extracts. Cross-reactive antibodies in this assay were subjected to expression in 1-liter scale followed by purification. Purified antibodies were tested for cross-reactivity in BIAcore™ and protease assays (Table 1).

[137] As shown in Table 1, a total of five different Fab cross-reactive with human and rat TIMP-1 were generated. BIAcore™ measurements revealed that although these antibodies clearly bind to human and rat TIMP-1, affinities for both species differ by at least a factor of 50. An antibody used for human therapy or in an animal model should have an affinity to the target protein in the low nanomolar, preferably in the sub-nanomolar range. As none of the above-described antibodies had affinities in this range for both species, these antibodies were not considered useful for further experiments or development.

EXAMPLE 16

Generation of blocking antibodies against human TIMP-1

[138] To generate blocking antibodies against human TIMP-1, the HuCAL®-Fab 1 library was used for antibody selection (AutoPan®) on purified TIMP-1 protein followed by subcloning and expression of the selected Fab fragments in *E. coli*. Crude antibody-containing *E. coli* extracts were used for primary antibody characterization in ELISA (AutoScreen®). Purified Fab proteins were subjected to further characterization in ELISA, TIMP-1/MMP-1 assay and BIAcore™. A total of 6100 clones were analyzed in AutoScreen®, 670 of them showed binding to human TIMP-1. Sequence analysis revealed that in total seven unique antibody clones had been selected (Table 2). For these seven Fab clones, the affinities measured in BIAcore™ were in the range of 10 – 180 nM (Table 4). When tested in the human protease assay, five of them were able to block the interaction between human TIMP-1 and MMP-1. The concentration of monovalent Fab needed to reverse the inhibitory effect of human TIMP-1 on human MMP-1 activity by 50% (IC₅₀) was in the range of 11 - 100 nM (Table 2). The most active Fab clones are MS-BW-3 (K_d 13 nM; IC₅₀ 11 nM) and MS-BW-28 (K_d 10 nM; IC₅₀ 22 nM).

[139] A striking feature of antibodies selected against human TIMP-1 is that they all exhibit the combination VH312 and a relatively short VH-CDR3 region, predominantly four amino acids (see Table 2). The HCDR3 cassettes assembled for the HuCAL®-Fab 1 library

were designed to achieve a length distribution ranging from 5 to 28 amino acid residues.

A four amino acid HCDR3 can occur in the library due to TRIM deletion, but is considered a very rare event. Another remarkable feature was the high degree of sequence homology among the selected LCDR3 sequences.

Table 2. Overview of adult-human TMF-1 Fab

Fab	Framework + CDR 3 sequence				Monovalent K _D	IC ₅₀ in human protease assay
	VH	HCDR3	VL	LCDR3		
MS-BW-1	H3	FMDI, SEQ ID NO:1	72	QSYDYGQFT, SEQ ID NO:44	65+/-13 nM ^a	>100 nM
MS-BW-2	H3	GFDY, SEQ ID NO:2	72	QSYDFKTYL, SEQ ID NO:45	180+/-28 nM	>100 nM
MS-BW-3	H3	FTDI, SEQ ID NO:3	72	QSYDFRFES, SEQ ID NO:46	13+/-2 nM	11+/-2 nM
MS-BW-25	H3	TFPFDADS, SEQ ID NO:4	72	QSYDFNVI, SEQ ID NO:47	25+/-16 nM	115+/-15 nM
MS-BW-26	H3	GHDVY, SEQ ID NO:5	72	QSYDFVRFM, SEQ ID NO:48	~100 nM	non blocking
MS-BW-27	H3	YWRGLSFDI, SEQ ID NO:6	72	QSYDFRFKFN, SEQ ID NO:49	~74	non blocking
MS-BW-28	H3	FFDY, SEQ ID NO:7	72	QSYDFRFES, SEQ ID NO:50	10+/-1 nM	22+/-20 nM

^a In cases where standard deviations are given, three independent measurements were done with Fab from three different protein expressions/purifications. ~ Indicates preliminary data, in cases where measurement was done only once.

EXAMPLE 17

Increasing the affinity of selected anti-human TIMP-1 antibodies

[140] In order to increase the affinity of monovalent anti-human TIMP-1 Fab fragments to the sub-nanomolar range, a step-wise affinity maturation approach was applied, by optimizing CDR sequences and keeping framework regions constant.

Affinity maturation by light chain cloning

[141] The CDR3 sequences of the two antibody fragments with highest affinity (MS-BW-3 and MS-BW-28) had the remarkable feature of an unusually short four amino acid HCDR3 sequence. Furthermore, each Fab had a very similar LCDR3 sequence. This indicates that MS-BW-3 and MS-BW-28 bind to the same epitope and that this epitope might tolerate only a very small subset of CDR3 sequences. As a four amino acid HCDR3 is a very rare event in the library, it can be anticipated that in the initial library not all possible combinations of the short HCDR3 and the preferred LCDR3 are present. Therefore, it was considered that another combination of the selected HCDR3 and LCDR3 sequences might increase the affinity. For this approach, the heavy chain of MS-BW-3 and MS-BW-28 were paired with the light chains of MS-BW-1, -2, -3, -25, -26, -27, and -28 by cloning.

[142] The resulting constructs were transformed into *E. coli* and expressions/purifications in 1-liter scale were performed. Of the 12 new constructs, 10 resulted in functional Fab molecules. These were analyzed in BIACore™ and human protease assay as summarized in Table 3. The best antibody named MS-BW-44 had a monovalent affinity of 2 nM and an IC₅₀ of 4 nM (FIG. 7) and was thus improved by a factor of 6.5 (K_d) or 2.75 (IC₅₀).

Table 3. Overview of Fab derived from light chain cloning

Fab	Framework + CDR 3 sequence				Monovalent K_D to human TIMP-1	IC_{50}^* in human protease assay
	VH	HCDR3	VL	LCDR3		
MS-BW-40	H3	FLDI, SEQ ID NO:3	72	QSYDYQQFT, SEQ ID NO:44	~49 nM	> 100 nM
MS-BW-41	H3	FLDI, SEQ ID NO:3	72	QSYDFKTYL, SEQ ID NO:45	~6 nM	29+/-6nM
MS-BW-43	H3	FLDI, SEQ ID NO:3	72	QSYDFINVI, SEQ ID NO:47	~65 nM	> 100 nM
MS-BW-44	H3	FLDI, SEQ ID NO:3	72	QSYDFVRFM, SEQ ID NO:48	2 +/- 0.4 nM*	4+/-1 nM
MS-BW-45	H3	FLDI, SEQ ID NO:3	72	QSYDFYKFN, SEQ ID NO:49	8 +/- 5 nM	9+/-3 nM
MS-BW-46	H3	FLDI, SEQ ID NO:3	72	QSYDFRRFS, SEQ ID NO:50	6 +/- 3 nM	4+/-0.5 nM
MS-BW-47	H3	FFDY, SEQ ID NO:7	72	QSYDYQQFT, SEQ ID NO:44	~152 nM	> 100 nM
MS-BW-49	H3	FFDY, SEQ ID NO:7	72	QSYDFKTYL, SEQ ID NO:45	~21 nM	> 100 nM
MS-BW-51	H3	FFDY, SEQ ID NO:7	72	QSYDFINVI, SEQ ID NO:47	~7 nM	7+/-1 nM
MS-BW-52	H3	FFDY, SEQ ID NO:7	72	QSYDFVRFM, SEQ ID NO:48	~11 nM	9+/-1 nM

* In cases where standard deviations are given, three independent measurements were done with Fab from three different protein expressions/purifications.

~ Indicates preliminary data, in cases where measurement was done only once.

Affinity maturation by optimizing HCDR1 and HCDR2

[143] In the HuCAL®-Fab 1 library, only the CDRs HCDR3 and LCDR3 are diversified to a high extent. Although it is known from crystallographic studies that amino acids from these two CDRs make most of the antibody antigen contacts, the residual four CDRs are also important for antigen binding. However, their contribution to the binding energy can vary from antibody to antibody. In the HuCAL®-Fab 1 library those CDRs exhibit only a limited variability due to the presence of the different master frameworks (Knappik *et al.*, 2000). In order to improve the affinity of the selected antibodies, an affinity maturation approach by randomizing HCDR1 and HCDR2 was applied. For this approach two affinity maturation libraries based on MS-BW-44 cloned into phage display vector pMORPH® 18 were created. In library 1, only HCDR2 of MS-BW-44 was diversified using "TRIM technology" as described in Virnekäs *et al.*, *Nucl. Acids. Res.* 22, 5600-07, 1994; Knappik *et al.*, *J. Mol. Biol.* 296, 57-86, 2000. In library 2, both HCDR1 and HCDR2 were diversified using the TRIM technology. In both cases, phage antibody libraries comprising 1×10^8 different clones were obtained. Both libraries were mixed and used as input for a modified AutoPan® procedure. In order to select antibodies having an increased affinity to human TIMP-1, solution panning using limiting amounts of biotinylated antigen and stringent washing conditions were applied. Antibody off rates were ranked by BIAcore™ using crude *E. coli* extracts of selected antibodies. Clones with slower off rate than parental clone MS-BW-44 were subjected to 1-liter scale expression and purification. Purified Fab were analyzed in BIAcore™ and human protease assay (Table 4).

Table 4. Comparison of Fab derived from HCDR1 and HCDR2 optimization with parental clone MS-BW-44

Fab	Monovalent K_D to human TIMP-1	IC_{50} in human protease assay*
MS-BW-44	2 +/- 0.4 nM	2 +/- 0.5 nM
MS-BW-44-2	0.5 +/- 0.2 nM	0.4 +/- 0.3 nM
MS-BW-44-6	0.6 +/- 0.2 nM	0.2 +/- 0.1 nM

* IC_{50} values derived from modified protease assay using decreased amounts of TIMP-1 and MMP-1 (0.4 nM each).

[144] Clone MS-BW-44-2 was derived from library 1 thus having a modified HCDR2 cassette. Its affinity measured by BIACORE™ was 0.5 nM. Clone MS-BW-44-6 was derived from library 2 having a modified HCDR 1 and HCDR 2 cassette and the affinity measured by BIACORE™ was 0.6 nM. A sequence comparison between the affinity matured antibodies and their parental clones is shown in Table 8.

Table 8: Overview and sequence comparison of affinity matured Fab fragments against human TIMP-1. Sequence changes compared to parental Fab fragments (**bold**) are italicized

Clone MS- BW-	VH				VL			Monov. K_d to human TIMP-1 (nM)	IC_{50} in human protease assay (nM)	
	Frame- work	HCDR1 sequence (SEQ ID NO:)	HCDR2 sequence (SEQ ID NO:)	HCDR3 sequence (SEQ ID NO:)	Framework	LCDR1 sequence (SEQ ID NO:)	LCDR2 sequence (SEQ ID NO:)	LCDR3 sequence (SEQ ID NO:)		
3	VH3	G F TFSSYAMS (355)	A I S G GGG S TYY A DSVK G (357)	F L DI (3)	VL2	T G TSS D VGG G NYV S (363)	D V SNRPS (364)	Q S Y D F L RPS (47)	13 +/- 2	11 +/- 2
44	VH3	G F TFSSYAMS (355)	A I S G GGG S TYY A DSVK G (357)	F L DI (3)	VL2	T G TSS D VGG G NYV S (363)	D V SNRPS (364)	Q S Y D P V R F M (48)	2 +/- 0.4	4 +/- 1
44-6	VH3	G F TFNSYAMS (356)	<i>V</i> I S G NG S NTYY A DSVK G (358)	F L DI (3)	VL2	T G TSS D VGG G NYV S (363)	D V SNRPS (364)	Q S Y D E V R F M (48)	0.6 +/- 0.2	0.2 +/- 0.1 *
44-2	VH3	G F TFSSYAMS (355)	<i>G</i> I S G NG V L I FY A DSVK G (359)	F L DI (3)	VL2	T G TSS D VGG G NYV S (363)	D V SNRPS (364)	Q S Y D E V R F M (48)	0.5 +/- 0.2	0.4 +/- 0.3 *
44-2-4	VH3	G F TFSSYAMS (355)	<i>G</i> I S G NG V L I FY A DSVK G (359)	G L MDY (360)	VL2	T G TSS D VGG G NYV S (363)	D V SNRPS (364)	Q S Y D F V R F M (48)	0.2 +/- 0.02	0.2 +/- 0.1 *
44-2-15	VH3	G F TFSSYAMS (355)	<i>G</i> I S G NG V L I FY A DSVK G (359)	R F D H (361)	VL2	T G TSS D VGG G NYV S (363)	D V SNRPS (364)	Q S Y D F V R F M (48)	0.3 +/- 0.1	0.2 +/- 0.1 *
44-2-16	VH3	G F TFSSYAMS (355)	<i>G</i> I S G NG V L I FY A DSVK G (359)	R F D V (362)	VL2	T G TSS D VGG G NYV S (363)	D V SNRPS (364)	Q S Y D P V R F M (48)	0.5 +/- 0.2	0.3 +/- 0.1 *
44-6-1	VH3	G F TFNSYAMS (356)	<i>V</i> I S G NG S NTYY A DSVK G (358)	F L DI (3)	VL2	T G TSS D VGG G NYV S (363)	D V SNRPS (364)	Q S Y D F I R F M (365)	0.2 +/- 0.04	0.2 +/- 0.1 *

* IC_{50} values derived from modified protease assay using decreased amounts of TIMP-1 and MMP-1; IC_{50} of MS-BW-44 is 2 nM under these conditions

[145] When initially analyzed in the human TIMP-1/MMP-1 assay, it was not possible to distinguish a Fab with a sub-nanomolar affinity from a Fab with 1 nM affinity, most likely because the concentration of Fab required to reverse the inhibitory effect of human TIMP-1 on human MMP-1 activity by 50% was below the concentration of total TIMP-1 and MMP-1 in the assay. When a modified assay was used with concentrations of TIMP-1 and MMP-1 decreased from 1.2 nM to 0.4 nM, it was possible to distinguish a 2 nM Fab from a sub-nanomolar Fab (Table 4, FIG. 8). Using this modified protease assay, MS-BW-44-2 and MS-BW-44-6 had IC₅₀ values of 0.4 nM and 0.2 nM respectively. Parental clone MS-BW-44 had an IC₅₀ of 2 nM under these conditions. Thus, by this affinity maturation approach, an affinity gain of a factor of 5 (K_d) or 5-10 (IC₅₀) was achieved.

Affinity maturation by optimizing HCDR3

[146] As mentioned above, amino acid residues in HCDR3 and LCDR3 are considered the most important for antigen binding. Taking into account that a four amino acid HCDR3 was not planned in the design of HuCAL®-Fab 1 and thus only occurs as a rare case due to a TRIM deletion, probably not all possible combinations of the four amino acids in HCDR3 were represented in the original HuCAL®-Fab 1 library. Therefore, an affinity maturation library was constructed with four and five amino acid HCDR3 maturation cassettes inserted into Fab derived from the previous maturation cycle (among them MS-BW-44-2 and MS-BW-44-6). The obtained affinity maturation library had a diversity of 1 × 10⁸ clones, therefore theoretically covering all possible four and five amino acid HCDR3 variations. Applying very stringent panning conditions, the best antibody identified, MS-BW-44-2-4, had an affinity measured by BLAcore™ of 0.2 nM and an IC₅₀ in human TIMP-1/MMP-1 assay of 0.2 nM. A sequence comparison between the affinity matured antibodies and their parental clones is shown in Table 8. The improvement factor gained by this affinity maturation approach is 2.5 with respect to the affinity and 2 with respect to the IC₅₀.

Affinity maturation by optimizing LCDR3

[147] As an alternative approach, a maturation strategy was used to further optimize the light chain CDR3 sequence. This was due to the fact that in the first maturation cycle where light chain exchange cloning between selected antibodies was applied, only a very limited subset of sequence variation had been exploited. Therefore, a maturation library was constructed in which, using TRIM technology, a diversified LCDR3 cassette was inserted into Fab, derived from HCDR1 and HCDR2 optimization (among them MS-BW-44-2 and MS-BW-44-6). The best Fab identified with this maturation strategy was MS-BW-44-6-1 with an affinity measured by BIAcore™ of 0.15 nM and an IC₅₀ in a human TIMP-1/MMP-1 assay of 0.2 nM. A sequence comparison between the affinity matured antibody and its parental clones is shown in Table 8. The improvement factor gained by this maturation approach is 4 with respect to affinity. A further improvement of the IC₅₀ in the protease assay could not be measured due to limitations in the assay.

[148] As a result of a step-wise affinity maturation approach using four different maturation strategies, the monovalent affinity of an anti-human TIMP-1 specific Fab fragment was improved by a factor of 87 and its activity in human TIMP-1/MMP-1 assay by a factor of 55. The decision for defining the best Fab fragment has been made on the basis of K_d measurements using BIAcore™, as this method proved to be reliable for ranking antibodies with sub-nanomolar affinities, whereas the sensitivity of the human TIMP-1/MMP-1 assay was considered not suitable to rank activity of the best Fabs in the sub-nanomolar range with respect to each other.

[149] The best Fab MS-BW-44-6-1 has an affinity measured by BIAcore™ of 0.15 nM and an IC₅₀ in human TIMP-1/MMP-1 assay of 0.2 nM. Compared to its parental clone, MS-BW-3, it has optimized LCDR3, HCDR1 and HCDR2 sequences.

EXAMPLE 18

Cross reactivity of selected anti-human TIMP-1 Fab with TIMP-2, TIMP-3, and TIMP-4

[150] TIMP-1 belongs to a family of closely related protease inhibitors all binding to various members of the MMP family of proteases. To date there are four human TIMP proteins described. To investigate potential cross-reactivity of antibody fragments selected against human TIMP-1 with other members of the human TIMP family, an ELISA was performed in which binding of antibody fragments to immobilized purified human TIMP-1, -2, -3 or -4 was analyzed (FIG. 10). Antibody fragments binding to immobilized human TIMP-1 showed no binding to human TIMP-2, -3, -4 above background level when compared to unrelated control protein BSA.

EXAMPLE 19

Generation of blocking antibodies against rat TIMP-1

[151] To generate blocking antibodies against rat TIMP-1, the HuCAL[®]-Fab 1 library was used for antibody selection (AutoPan[®]) on immobilized rat TIMP-1 followed by subcloning and expression of the selected Fab fragments in *E. coli*. Crude antibody-containing *E. coli* extracts were used for primary antibody characterization in ELISA (AutoScreen[®]). Purified Fab proteins were subjected to further characterization in ELISA, protease assays, and BiACoreTM. Of the 8,450 selected clones were analyzed in AutoScreen[®], 750 of them showed binding to rat TIMP-1. Sequence analysis revealed that in total 36 unique Fab clones specific for rat TIMP-1 were enriched during selection (Table 7). Their affinities were measured by BiACoreTM and were found to be in the range of 9 – 1000 nM (Table 7). When tested in the rat protease assay, all but one of them were able to block the interaction between rat TIMP-1 and rat MMP-13 (Table 7). The concentration of monovalent Fab needed to reverse the inhibitory effect of rat TIMP-1 on rat MMP-13 activity by 50% (IC₅₀) was in the range of 7 - 300 nM. The most active Fab

clones are MS-BW-14 (K_d 10 nM; IC_{50} 14 nM), MS-BW-17 (K_d 13 nM; IC_{50} 11 nM), and MS-BW-54 (K_d 9 nM; IC_{50} 7 nM).

Table 7. Overview of anti-rat TIMP-1 Fab

Fab	Framework + CDR 3 sequence				Monovalent K_D to rat TIMP-1	IC_{50}^* in rat protease assay
	VH	HCDR3	VL	LCDR3		
MS-BW-5	H1A	GLYWAVYPYPDF, SEQ ID NO:8	?1	QSRDFNRGP, SEQ ID NO:51	~210 nM	non blocking
MS-BW-6	H3	LDTYYPDLFDY, SEQ ID NO:9	?1	QSYDQRKW, SEQ ID NO:52	~68 nM	~100 nM
MS-BW-7	H1A	TYYYFDS, SEQ ID NO:10	?3	QQLYGTVS, SEQ ID NO:53	~168 nM	> 300 nM
MS-BW-9	H3	YMAYMAEAIDV, SEQ ID NO:11	?1	QSYDGFKTH, SEQ ID NO:54	~256 nM	> 300 nM
MS-BW-10	H1B	LVGIVGYKPDELLYFDV, SEQ ID NO:12	?3	QSYDYSLL, SEQ ID NO:55	~200 nM	~ 30 nM
MS-BW-11	H3	YGAYFGLDY, SEQ ID NO:13	?3	QSYDFNFH, SEQ ID NO:56	~200 nM	>300 nM
MS-BW-12	H6	GYADISFDY, SEQ ID NO:14	?2	QSYDMIARYP, SEQ ID NO:57	~419 nM	>300 nM
MS-BW-13	H3	YYLLLLDY, SEQ ID NO:15	?3	QSWDIHPFDV, SEQ ID NO:58	~939 nM	not tested
MS-BW-14	H1A	WSDQSYHYYWHPYFDV, SEQ ID NO:16	?1	QSWDLEPY, SEQ ID NO:59	10 +/- 5 nM	14 +/- 3 nM
MS-BW-15	H3	LIGYFDL, SEQ ID NO:17	?2	QSYDVLDE, SEQ ID NO:60	~80 nM	~ 200 nM
MS-BW-17	H5	LTNYFDSDIYYDH, SEQ ID NO:18	?2	QSYDPSHPSK, SEQ ID NO:61	13 +/- 3 nM	11 +/- 3 nM
MS-BW-18	H5	LVGGGYDLMFDS, SEQ ID NO:19	?2	QSYDDMMQF, SEQ ID NO:62	~153 nM	> 300 nM
MS-BW-19	H5	YVTYGYDDYHFDY, SEQ ID NO:20	?2	QSWDINHAI, SEQ ID NO:63	~187 nM	> 300 nM
MS-BW-20	H1A	SGYLDY, SEQ ID NO:21	?2	QSYDYYDYG, SEQ ID NO:64	~70 nM	> 300 nM

MS-BW-21	H1A	YIGYTNVMDIRPGYFLDY, SEQ ID NO:22	?3	QQANDFPI, SEQ ID NO:65	36 +/- 2 nM	67 +/- 5 nM
MS-BW-22	H5	FRAYGDDFYFDV, SEQ ID NO:23	?2	QSWDNLKMPV, SEQ ID NO:66	35 nM	65 +/- 11 nM
MS-BW-23	H1B	JMWSDYQQLVKGGDI, SEQ ID NO:24	?2	QSYDVFPINR, SEQ ID NO:67	~207 nM	> 300 nM
MS-BW-24	H5	YYVTDTAYFDY, SEQ ID NO:25	?2	QSDLYFP, SEQ ID NO:68	23 nM	20 +/- 1 nM
MS-BW-29	H5	HDFDGSIFMDF, SEQ ID NO:26	?2	QSYDVTPR, SEQ ID NO:69	~214 nM	>100 nM
MS-BW-30	H5	YAGHQYEFFDF, SEQ ID NO:27	?3	QSRDPVGFP, SEQ ID NO:70	~36 nM	>100 nM
MS-BW-31	H5	LYADADIYFDY, SEQ ID NO:28	?2	QSYDLSPR, SEQ ID NO:71	~13 +/- 9 nM	>100 nM
MS-BW-32	H1A	TKYVGSEDV, SEQ ID NO:29	?2	QSYDFSHYFF, SEQ ID NO:72	~92 nM	> 100 nM
MS-BW-36	H5	YRYPHMFDF, SEQ ID NO:30	?3	QSYDLRYSH, SEQ ID NO:73	~42 nM	~75 nM
MS-BW-37	H5	LFAGLELYFDY, SEQ ID NO:31	?2	QSYDLRNR, SEQ ID NO:74	10 +/- 9 nM	>100 nM
MS-BW-38	H3	GGFFNMDY, SEQ ID NO:32	?2	QSYDFTYGS, SEQ ID NO:75	~353 nM	>300 nM
MS-BW-39	H1A	GYIPYHLDY, SEQ ID NO:33	?3	QQFNNDSPY, SEQ ID NO:76	~108 nM	>100 nM
MS-BW-54	H5	YYGFEYDLLFDN, SEQ ID NO:34	?2	QSYDISGYP, SEQ ID NO:77	9 +/- 1 nM	7 nM
MS-BW-55	H1B	ITYIGYDF, SEQ ID NO:35	?2	QSRDLYYVYY, SEQ ID NO:78	~23 nM	~ 100 nM
MS-BW-56	H1A	QEWWMDY, SEQ ID NO:36	?3	QSYDRSMW, SEQ ID NO:79	~170 nM	> 100 nM
MS-BW-57	H5	LYPEDLIYFDY, SEQ ID NO:37	?2	QSWDVTQTDK, SEQ ID NO:80	~39 nM	~60 nM
MS-BW-58	H6	WMTPPGHYYGYTFDV, SEQ ID NO:38	?3	QSWDPSHYY, SEQ ID NO:81	~138 nM	not tested
MS-BW-59	H5	LRVHDYAMYFDL, SEQ ID NO:39	?2	QSYDIMPER, SEQ ID NO:82	~15 nM	30 +/- 5 nM

MS-BW-60	H5	IVFSYNGSVPYFDY, SEQ ID NO:40	? 2	QSMDFRLMH, SEQ ID NO:83	~30 nM	> 100 nM
MS-BW-61	H5	IIGDYVIFFDV, SEQ ID NO:41	? 2	QSFDMIHPY, SEQ ID NO:84	~51 nM	> 100 nM
MS-BW-62	H5	LFTYYPFLYFDV, SEQ ID NO:42	? 2	QSDFPVM, SEQ ID NO:85	~36 nM	19 +/- 2
MS-BW-63	H5	ILTGHVLLFDY, SEQ ID NO:43	? 2	QSDNPYI, SEQ ID NO:86	~14 nM	20 +/- 1 nM

* In cases where standard deviations are given, three independent measurements were done with Fab from three different protein expressions/purifications.

~ Indicates preliminary data, in cases where measurement was done only once.

EXAMPLE 20

Increasing the affinity of selected anti-rat TIMP-1 antibodies

[152] Affinity maturation was applied to increase the affinity of monovalent anti-rat TIMP-1 Fab fragments to the sub-nanomolar range. No clear sequence homology could be identified among the light chain CDR3 sequences of the selected antibody fragments, indicating that an optimal light chain CDR3 sequence was probably not present or had not been selected from the original HuCAL®-Fab 1 library. We therefore started with modification of LCDR3 to increase the affinity of Fab's.

[153] Two affinity maturation libraries based on MS-BW-14, -17, and -54 cloned into phage display vector pMORPH® 18 were created. In library 1, only LCDR3 was diversified using TRIM technology, as described in Vimetas et al., *Nucl. Acids. Res.* 22, 5600-07, 1994; Knappik et al., *J. Mol. Biol.* 296, 57-86, 2000. In library 2, LCDR1, LCDR2, and LCDR3 were diversified simultaneously using the TRIM technology, while the connecting framework regions were kept constant. In both cases, phage antibody libraries comprising 3×10^8 different clones were obtained. Both libraries were mixed and used as input for a modified AutoPan® procedure. To select antibodies having an increased affinity to rat TIMP-1, solution panning using limiting amounts of biotinylated antigen and stringent washing conditions were applied.

[154] Antibody-off-rates were ranked by BIAcore™ using crude *E. coli* extracts. Clones with slower off rate than parental clones MS-BW-14, -17, or -54 were subjected to expression and purification in 1-liter scale. Purified Fab were analyzed in BIAcore™ and rat protease assays (Table 6). MS-BW-17-1 (K_d 0.8 nM, IC_{50} 1.6 nM), MS-BW-17-2 (K_d 1.3 nM, IC_{50} 1.1 nM), and MS-BW-17-3 (K_d 1.9 nM, IC_{50} 3 nM) were derived from affinity maturation library 1 having an optimized LCDR3 sequence, whereas MS-BW-

54-1 (K_d 2 nM, IC_{50} 3 nM) was derived from affinity maturation library 2 having an optimized LCDR1, -2, and -3 sequence (Table 9).

Table 9. Overview and sequence comparison of affinity matured Fab fragments against rat TIMP-1. Sequence changes compared to parental Fab fragments (**bold**) are italicized.

Clone (MS- BW-)	VH				VL				Monov. K_D to rat TIMP-1 (nM)	IC ₅₀ in rat protease assay (nM)
	Frame- work	HCDR1 sequence (SEQ ID NO:)	HCDR2 sequence (SEQ ID NO:)	HCDR3 sequence (SEQ ID NO:)	Frame- work	LCDR1 sequence (SEQ ID NO:)	LCDR2 sequence (SEQ ID NO:)	LCDR3 sequence (SEQ ID NO:)		
14	VH1A	GGTFSSYAI S (366)	GI IPIFI G TANIAQ K PFQG (368)	WSDQ S YHYIWH P YFD V	VL1	SG SSSNIGSNYVS (371)	L MIYDNN Q RPS (373)	Q SWD L E P Y (59)	10 +/- 5	14 +/- 3
17	VH5	GY SFTSYWIG (367)	II YPG D SD T RYSP S FQG (369)	L TNYF D SIYYDH (18)	VL2	T GTSSD V GG Y NYVS (363)	L MIYD V SNRPS (374)	Q SYD P SH P S X (61)	13 +/- 3	11 +/- 3
54	VH5	GY SFTSYWIG (367)	II YPG D SD T RYSP S FQG (369)	Y YG F EY D LL F DN (34)	VL2	T GTSSD V GG Y NYVS (363)	L MIYD V SNRPS (374)	Q SYD I S G Y (77)	9 +/- 1	7
17-1	VH5	GY SFTSYWIG (367)	II YPG D SD T RYSP S FQG (369)	L TNYF D SIYYDH (18)	VL2	T GTSSD V GG Y NYVS (363)	L MIYD V SNRPS (374)	Q AF D VAP N G X (376)	0.8	1.6
17-2	VH5	GY SFTSYWIG (367)	II YPG D SD T RYSP S FQG (369)	L TNYF D SIYYDH (18)	VL2	T GTSSD V GG Y NYVS (363)	L MIYD V SNRPS (374)	Q AF A V M F V S (377)	1.3	1.1
17-3	VH5	GY SFTSYWIG (367)	II YPG D SD T RYSP S FQG (369)	L TNYF D SIYYDH (18)	VL2	T GTSSD V GG Y NYVS (363)	L MIYD V SNRPS (374)	Q SP T VS P GA D (378)	1.9	3
54-1	VH5	GY SFTSYWIG (367)	II YPG D SD T RYSP S FQG (369)	Y GF E Y D LL F DN (34)	VL2	T GTSSD I GG Y NYVS (372)	L MIYAG C RPS (375)	Q AYD S SG Y (379)	2	3

[155] The improvement gained by these different one-step maturation strategies was up to a factor of 16.3 with regard to affinity and 10 with regard to functional activity in the protease assay.

EXAMPLE 21

Conversion of anti-TIMP-1 Fab fragments into human IgG₁ molecules for use in the rat model of chronic carbon tetrachloride-induced liver fibrosis

[156] Anti-TIMP-1 Fab fragments were converted into human IgG₁ molecules to create antibody molecules with prolonged *in vivo* half-lives for the use in the rat model of chronic carbon tetrachloride-induced liver fibrosis. This was done by cloning the heavy and light chain variable regions of the Fab into two separate vectors for mammalian IgG₁ expression (Krebs *et al.*, 2001)

[157] Anti-rat TIMP-1 clone MS-BW-14 was chosen for the first *in vivo* study, and IgG₁ protein was produced by transient expression. Anti-human TIMP-1 clone MS-BW-3 was selected as a negative control IgG₁ and was also produced by transient expression. Purified IgG₁ proteins MS-BW-14 and MS-BW-3 were subjected to quality control in BIAcore™ and rat TIMP-1/rat MMP-13 assays. Bivalent affinity for rat TIMP-1 measured in BIAcore™ (chip density 500 RU, fitting model for bivalent analyte) is 0.2 nM for MS-BW-14, compared to 13 nM for the corresponding monovalent Fab fragment. This increase in affinity for the IgG₁ is due to the avidity effects caused by binding of bivalent IgG₁ to immobilized rat TIMP-1 protein on the BIAcore™ chip. As expected, the negative control IgG₁ MS-BW-3 showed no binding to rat TIMP-1 but bound to human TIMP-1 with a bivalent affinity of approximately 0.4 nM.

[158] FIG. 12 shows the activity of MS-BW-14 Fab and IgG₁ and MS-BW-3 IgG₁ in a rat TIMP-1/rat MMP-13 assay. The IC₅₀ of MS-BW-14 Fab and IgG₁ are nearly identical. The avidity effect seen in BIAcore™ does not occur in this assay because, in contrast to

the BIAcore™ experiment, this assay is based on a monovalent interaction in solution between TIMP-1 and the IgG₁. As expected, MS-BW-3 has no effect on rat TIMP-1 binding to rat MMP-13 and thus is a suitable negative control for a rat *in vivo* study.

[159] Affinity matured clone MS-BW-17-1 was then converted from a monovalent Fab fragment to a bivalent IgG₁. Protein was produced by stable transfection. Purified protein was subjected to quality control in BIAcore™ and rat TIMP-1/rat MMP-13 assays (FIG. 13). In BIAcore™ an increased bivalent affinity (avidity) of 0.04 nM for IgG₁ compared to 0.8 nM for monovalent Fab fragment was seen, whereas the activity in the rat TIMP-1/rat MMP-13 assay was comparable for IgG₁ and Fab as expected.

EXAMPLE 22

Cross-reactivity of anti-rat TIMP-1 IgG, MS-BW-17-1 with mouse TIMP-1

[160] Species cross-reactivity of MS-BW-17-1 IgG₁ and Fab with mouse TIMP-1 was determined by BIAcore™ to investigate the feasibility of alternative *in vivo* models that use mice instead of rats. Although MS-BW-17-1 clearly bound to mouse TIMP-1 immobilized to the chip surface, the affinity of both Fab (180 nM) and IgG₁ (9 nM) was 225-fold weaker than the affinity to rat TIMP-1. As the interaction between mouse TIMP-1 and BW-17-1 IgG₁ in serum is most likely monovalent, the affinity of BW-17-1 Fab probably reflects the "real" affinity of this interaction. Therefore, the Fab affinity value should be considered when calculating the feasibility of using BW-17-1 IgG₁ in a mouse *in vivo* study.

EXAMPLE 23

Effect of Timp-1 antibody on the development of bleomycin-induced pulmonary fibrosis

[161] The following example demonstrates the ability of a human anti-rat Timp-1 antibody (BW7.1) to prevent fibrotic collagen deposition in a bleomycin-induced rat lung fibrosis model.

[162] Male Lewis rats (6 weeks of age) received a single intratracheal challenge with bleomycin (0.3 mg/rat, in saline) or vehicle (saline) on day 0. Fourteen days later, animals were euthanized, the lung excised, fixed, and processed for evaluation of lung fibrosis. Lung tissue sections were cut, and quantitative assessment by image analysis of lung collagen in lung tissue sections stained with Mason Trichrome stain performed.

[163] Antibody administration: A 20 mg/kg dose of human anti-rat TIMP-1 antibody or control human antibody (IgG) was administered subcutaneously on day -1. Subsequently, a 10mg/kg dose of human anti-rat TIMP-1 antibody or control human antibody (IgG) was administered s.c. on days 2, 5, 8, and 11. The following five groups of animals were studied: Saline i.t. challenge + antibody vehicle (PBS); Saline i.t. challenge + TIMP-1 antibody; Bleomycin i.t. challenge + TIMP-1 antibody; Bleomycin i.t. challenge + antibody vehicle (PBS); Bleomycin i.t. challenge + control antibody.

[164] FIG. 14 shows the effect of the inhibitory effect of TIMP-1 antibody on bleomycin-induced lung fibrotic collagen.

EXAMPLE 24

Effect of BW-14 anti-TIMP-1 antibody in a rat model with CCl₄-induced liver fibrosis

[165] Carbon tetrachloride (CCl₄) was used to induce liver fibrosis as described in Example 9. A single intravenous dose of 3 mg/kg BW-14 or control antibody BW-3, respectively,

was administered on day 19. At this time, total liver collagen (hydroxyproline determined according to Prockop and Udenfried) is already significantly increased by CCl₄, and fibrotic collagen rapidly accumulates during the following weeks. The rats were sacrificed on day 28. The treatment groups were: no CCl₄ + control antibody BW 3 (n=10 rats), CCl₄ + control antibody BW 3 (n=20 rats), and CCl₄ + BW 14 (n=20 rats).

[166] The effect of control vs. TIMP-1 antibody as reflected in morphometric measurements of fibrous collagen (Sirius Red stained area as percentage of the total field) is shown in FIG. 15. Comparison of both control antibody treated groups shows that CCl₄ caused an approximately three-fold increase in collagen area. BW-14 antibody treatment reduced the pathological collagen increment by 26%. The lower fibrous collagen value of the CCl₄ + BW-14 group compared to the CCl₄ + BW-3 group was statistically significant (p< 0.05, Kolmogorow-Smirnow test).

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CLAIMS

1. A purified preparation of a human antibody, wherein the antibody:
binds to a tissue inhibitor of metalloprotease-1 (TIMP-1); and
neutralizes a matrix metalloprotease (MMP)-inhibiting activity of the TIMP-1.
2. The preparation of claim 1 wherein the MMP is human MMP-1.
3. The preparation of claim 2 wherein the MMP is rat MMP-13.
4. The preparation of claim 1 wherein the TIMP-1 is a human TIMP-1.
5. The preparation of claim 4 wherein the antibody binds to the human TIMP-1 with
a K_d selected from the group consisting of about 0.1 nM to about 10 μ M, about 2 nM to
about 1 μ M, about 2 nM to about 200 nM, about 2 nM to about 150 nM, about 50 nM to
about 100 nM, about 0.2 nM to about 13 nM, about 0.2 nM to about 0.5 nM, about 2 nM to
about 13 nM, and about 0.5 nM to about 2 nM.
6. The preparation of claim 4 wherein the antibody binds to the human TIMP-1 with
a K_d selected from the group consisting of about 0.2 nM, about 0.3 nM, about 0.5 M, about
0.6 nM, about 2 nM, about 7 nM, about 10 nM, about 11 nM, and about 13 nM.
7. The preparation of claim 4 wherein the antibody neutralizes the MMP-inhibiting
activity of the human TIMP-1 with an IC_{50} selected from the group consisting of about .1 nM
to about 200 nM, about 1 nM to about 100 nM, about 2 nM to about 50 nM, about 5 nM to
about 25 nM, about 10 nM to about 15 nM, about 0.2 nM to about 11 nM, about 0.2 nM to
about 4 nM, and about 4 nM to about 11 nM.

8. The preparation of claim 4 wherein the antibody neutralizes the MMP-inhibiting activity of the human TIMP-1 with an IC_{50} selected from the group consisting of about 0.2 nM, about 0.3 nM, about 0.4 nM, about 4 nM, about 7 nM, about 9 nM, and about 11 nM.

9. The preparation of claim 4 wherein the K_d for binding to human TIMP-1 and the IC_{50} for neutralizing the MMP-inhibiting activity of the human TIMP-1 are approximately equal.

10. The preparation of claim 1 wherein the TIMP-1 is a rat TIMP-1.

11. The preparation of claim 10 wherein the antibody binds to the rat TIMP-1 with a K_d selected from the group consisting of about 0.1 nM to about 10 μ M, about 2 nM to about 1 μ M, about 2 nM to about 200 nM, about 2 nM to about 150 nM, about 50 nM to about 100 nM, about 1.3 nM to about 13 nM, about 1.8 nM to about 10 nM, about 2 nM to about 9 nM, about 1.3 nM to about 9 nM, and about 2 nM to about 10 nM.

12. The preparation of claim 10 wherein the antibody binds to the rat TIMP-1 with a K_d selected from the group consisting of about 0.8 nM, about 1 nM, about 1.3 nM, about 1.9 nM, about 2 nM, about 3 nM, about 9 nM, about 10 nM, about 13 nM, about 14 nM, and about 15 nM.

13. The preparation of claim 10 wherein the antibody neutralizes the rat TIMP-1 activity with an IC_{50} selected from the group consisting of about .1 nM to about 300 nM, about 1 nM to about 100 nM, about 2 nM to about 50 nM, about 5 nM to about 25 nM, about 10 nM to about 15 nM, about 1.1 nM to about 14 nM, about 1.6 nM to about 11 nM, about 3

nM to about 7 nM, about 1.1 nM to about 7 nM, about 1.1 nM to about 11 nM, about 3 nM to about 11 nM, and about 3 nM to about 14 nM.

14. The preparation of claim 10 wherein the antibody neutralizes the rat TIMP-1 activity with an IC₅₀ selected from the group consisting of about 1.1 nM, about 1.6 nM, about 3 nM, about 7 nM, about 11 nM, about 14 nM, about 19 nM, about 20 nM, about 30 nM, and about 100 nM.

15. The preparation of claim 10 wherein the K_d for binding to rat TIMP-1 and the IC₅₀ for neutralizing the MMP-inhibiting activity of the rat TIMP-1 are approximately equal.

16. A purified preparation of a human antibody which comprises a VHCDR3 region comprising an amino acid sequence selected from the group consisting of SEQ ID NOS:1-43 and 360.

17. A purified preparation of a human antibody which comprises a VLCDR3 region comprising an amino acid sequence selected from the group consisting of SEQ ID NOS:44-86 and 365-379.

18. A purified preparation of a human antibody which comprises a VHCDR3 and VLCDR3 amino acid sequence pair selected from the group consisting of SEQ ID NOS:1 and 44, SEQ ID NOS:2 and 45, SEQ ID NO:3 and 46, SEQ ID NOS:4 and 47, SEQ ID NOS:5 and 48, SEQ ID NOS:6 and 49, SEQ ID NOS:7 and 50, SEQ ID NOS:3 and 44, SEQ ID NOS:3 and 45, SEQ ID NOS:3 and 47, SEQ ID NOS:3 and 48, SEQ ID NOS:3 and 49, SEQ ID NOS:3 and 50, SEQ ID NOS:7 and 44, SEQ ID NOS:7 and 45, SEQ ID NOS:7 and 47, SEQ ID NOS:7 and 48, SEQ ID NOS:8 and 51, SEQ ID NOS:9 and 52, SEQ ID NOS:10

and 53, SEQ ID NOS:11 and 54, SEQ ID NOS:12 and 55, SEQ ID NOS:13 and 56, SEQ ID NOS:14 and 57, SEQ ID NOS:15 and 58, SEQ ID NOS:16 and 59, SEQ ID NOS:17 and 60, SEQ ID NOS:18 and 61, SEQ ID NOS:19 and 62, SEQ ID NOS:20 and 63, SEQ ID NOS:21 and 64, SEQ ID NOS:22 and 65, SEQ ID NOS:23 and 66, SEQ ID NOS:24 and 67, SEQ ID NOS:25 and 68, SEQ ID NOS:26 and 69, SEQ ID NOS:27 and 70, SEQ ID NOS:28 and 71, SEQ ID NOS:29 and 72, SEQ ID NOS:30 and 73, SEQ ID NOS:31 and 74, SEQ ID NOS:32 and 75, SEQ ID NOS:33 and 76, SEQ ID NOS:34 and 77, SEQ ID NOS:35 and 78, SEQ ID NOS:36 and 79, SEQ ID NOS:37 and 80, SEQ ID NOS:38 and 81, SEQ ID NOS:39 and 82, SEQ ID NOS:40 and 83, SEQ ID NOS:41 and 84, SEQ ID NOS:42 and 85, SEQ ID NOS:43 and 86, SEQ ID NOS:3 and 48, SEQ ID NOS:360 and 48, SEQ ID NOS:3 and 365, SEQ ID NOS:16 and 59, SEQ ID NOS:18 and 61, SEQ ID NOS:34 and 77, SEQ ID NOS:34 and 379, SEQ ID NOS:18 and 376, SEQ ID NOS:18 and 377, and SEQ ID NOS:18 and 378.

19. A purified preparation of a human antibody comprising a VHCDR3 and VLCDR3 amino acid sequence pair selected from the group consisting of SEQ ID NOS:1 and 44, SEQ ID NOS:2 and 45, SEQ ID NO:3 and 46, SEQ ID NOS:4 and 47, SEQ ID NOS:5 and 48, SEQ ID NOS:6 and 49, SEQ ID NOS:7 and 50, SEQ ID NOS:3 and 44, SEQ ID NOS:3 and 45, SEQ ID NOS:3 and 47, SEQ ID NOS:3 and 48, SEQ ID NOS:3 and 49, SEQ ID NOS:3 and 50, SEQ ID NOS:7 and 44, SEQ ID NOS:7 and 45, SEQ ID NOS:7 and 47, SEQ ID NOS:7 and 48, SEQ ID NOS:8 and 51, SEQ ID NOS:9 and 52, SEQ ID NOS:10 and 53, SEQ ID NOS:11 and 54, SEQ ID NOS:12 and 55, SEQ ID NOS:13 and 56, SEQ ID NOS:14 and 57, SEQ ID NOS:15 and 58, SEQ ID NOS:16 and 59, SEQ ID NOS:17 and 60, SEQ ID

NOS:18 and 61, SEQ ID NOS:19 and 62, SEQ ID NOS:20 and 63, SEQ ID NOS:21 and 64, SEQ ID NOS:22 and 65, SEQ ID NOS:23 and 66, SEQ ID NOS:24 and 67, SEQ ID NOS:25 and 68, SEQ ID NOS:26 and 69, SEQ ID NOS:27 and 70, SEQ ID NOS:28 and 71, SEQ ID NOS:29 and 72, SEQ ID NOS:30 and 73, SEQ ID NOS:31 and 74, SEQ ID NOS:32 and 75, SEQ ID NOS:33 and 76, SEQ ID NOS:34 and 77, SEQ ID NOS:35 and 78, SEQ ID NOS:36 and 79, SEQ ID NOS:37 and 80, SEQ ID NOS:38 and 81, SEQ ID NOS:39 and 82, SEQ ID NOS:40 and 83, SEQ ID NOS:41 and 84, SEQ ID NOS:42 and 85, SEQ ID NOS:43 and 86, SEQ ID NOS:3 and 48, SEQ ID NOS:360 and 48, SEQ ID NOS:3 and 365, SEQ ID NOS:16 and 59, SEQ ID NOS:18 and 61, SEQ ID NOS:34 and 77, SEQ ID NOS:34 and 379, SEQ ID NOS:18 and 376, SEQ ID NOS:18 and 377, and SEQ ID NOS:18 and 378.

20. The purified preparation of claim 19 wherein the human antibody comprises a heavy chain having an amino acid sequence selected from the group consisting of SEQ ID NOS:140-182.

21. The purified preparation of claim 19 wherein the human antibody comprises a light chain having an amino acid sequence selected from the group consisting of SEQ ID NOS:97-139.

22. A purified preparation of a human antibody which comprises a heavy chain and a light chain amino acid pair selected from the group consisting of SEQ ID NOS:140 and 97, SEQ ID NOS:141 and 98, SEQ ID NOS:142 and 99, SEQ ID NOS:143 and 100, SEQ ID NOS:144 and 101, SEQ ID NOS:145 and 102, SEQ ID NOS:146 and 103, SEQ ID NOS:142 and 97, SEQ ID NOS:142 and 98, SEQ ID NOS:142 and 100, SEQ ID NOS:142 and 101,

SEQ ID NOS:142 and 102, SEQ ID NOS:142 and 103, SEQ ID NOS:146 and 97, SEQ ID NOS:146 and 98, SEQ ID NO:146 and 100, SEQ ID NOS:146 and 101, SEQ ID NOS:148 and 104, SEQ ID NOS:148 and 105, SEQ ID NOS:149 and 106, SEQ ID NOS:150 and 107, SEQ ID NOS:151 and 108, SEQ ID NOS:152 and 109, SEQ ID NOS:153 and 110, SEQ ID NOS:154 and 111, SEQ ID NOS:155 and 112, SEQ ID NOS:156 and 113, SEQ ID NOS:157 and 114, SEQ ID NOS:158 and 115, SEQ ID NOS:159 and 116, SEQ ID NOS:160 and 117, SEQ ID NOS:161 and 118, SEQ ID NOS:162 and 119, SEQ ID NOS:163 and 120, SEQ ID NOS:164 and 121, SEQ ID NOS:165 and 122, SEQ ID NOS:166 and 123, SEQ ID NOS:167 and 124, SEQ ID NOS:168 and 125, SEQ ID NOS:169 and 126, SEQ ID NOS:170 and 127, SEQ ID NOS:171 and 128, SEQ ID NOS:172 and 129, SEQ ID NOS:173 and 130, SEQ ID NOS:174 and 131, SEQ ID NOS:175 and 132, SEQ ID NOS:176 and 133, SEQ ID NOS:177 and 134, SEQ ID NOS:178 and 135, SEQ ID NOS:179 and 136, SEQ ID NOS:180 and 137, SEQ ID NOS:181 and 138, and SEQ ID NOS:182 and 139.

23. A pharmaceutical composition comprising:
 - a human antibody which (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1; and
 - a pharmaceutically acceptable carrier.
24. The pharmaceutical composition of claim 23 wherein the MMP is human MMP-1.
25. The pharmaceutical composition of claim 23 wherein the MMP is rat MMP-13.
26. The pharmaceutical composition of claim 23 wherein the TIMP-1 is a human TIMP-1.

27. The pharmaceutical composition of claim 23 wherein the TIMP-1 is a rat TIMP-1.
28. The pharmaceutical composition of claim 23 wherein a K_d for binding to the TIMP-1 and an IC_{50} for neutralizing the MMP-1-inhibiting activity of the TIMP-1 are approximately equal.
29. A purified polynucleotide which encodes a human antibody comprising a VHCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:1-43 and 360, wherein the human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1.
30. The purified polynucleotide of claim 31 wherein the VHCDR3 region is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:227-269.
31. A purified polynucleotide which encodes a human antibody comprising a VLCDR3 region which comprises an amino acid sequence selected from the group consisting of SEQ ID NOS:44-86 and 365-379, wherein the human antibody (1) binds to a TIMP-1 and (2) neutralizes an MMP-inhibiting activity of the TIMP-1.
32. The purified polynucleotide of claim 31 wherein the VLCDR3 region is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:184-226.
33. The purified polynucleotide of claim 31 wherein the human antibody comprises a heavy chain having an amino acid sequence selected from the group consisting of SEQ ID NOS:140-182.
34. The purified polynucleotide of claim 33 wherein the heavy chain is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:269-311.

35. The purified polynucleotide of claim 33 wherein the human antibody comprises a light chain having an amino acid sequence selected from the group consisting of SEQ ID NOS:97-139.
36. The purified polynucleotide of claim 35 wherein the light chain is encoded by a nucleotide sequence selected from the group consisting of SEQ ID NOS:312-354.
37. An expression vector comprising the polynucleotide of claim 29.
38. An expression vector comprising the polynucleotide of claim 30.
39. An expression vector comprising the polynucleotide of claim 31.
40. An expression vector comprising the polynucleotide of claim 32.
41. An expression vector comprising the polynucleotide of claim 33.
42. An expression vector comprising the polynucleotide of claim 34.
43. An expression vector comprising the polynucleotide of claim 35.
44. An expression vector comprising the polynucleotide of claim 36.
45. A host cell comprising the expression vector of claim 37.
46. A host cell comprising the expression vector of claim 38.
47. A host cell comprising the expression vector of claim 39.
48. A host cell comprising the expression vector of claim 40.
49. A host cell comprising the expression vector of claim 41.
50. A host cell comprising the expression vector of claim 42.
51. A host cell comprising the expression vector of claim 43.
52. A host cell comprising the expression vector of claim 44.

53. A method of making a human antibody, comprising the steps of:
 - culturing the host cell of claim 45 under conditions whereby the antibody is expressed; and
 - purifying the human antibody from the host cell culture.
54. The method of claim 55 wherein the expression vector comprises a polynucleotide sequence selected from the group consisting of SEQ ID NOS:183-357.
55. A method of decreasing an MMP-inhibiting activity of a TIMP-1, comprising the step of:
 - contacting the TIMP-1 with a human antibody that binds to the TIMP-1, whereby the MMP-inhibiting activity of the TIMP-1 is decreased relative to MMP-inhibiting activity of the TIMP-1 in the absence of the antibody.
56. The method of claim 55 wherein the MMP is human MMP-1.
57. The method of claim 55 wherein the MMP is rat MMP-13.
58. The method of claim 55 wherein the TIMP-1 is a human TIMP-1.
59. The method of claim 55 wherein the TIMP-1 is a rat TIMP-1.
60. The method of claim 55 wherein the step of contacting is carried out in a cell-free system.
61. The method of claim 55 wherein the step of contacting is carried out in a cell culture system.
62. The method of claim 55 wherein the step of contacting is carried out *in vivo*.

63. The method of claim 55 wherein the antibody comprises a VHCDR3 and a VLCDR3 amino acid sequence pair selected from the group consisting of SEQ ID NOS:1 and 44, SEQ ID NOS:2 and 45, SEQ ID NO:3 and 46, SEQ ID NOS:4 and 47, SEQ ID NOS:5 and 48, SEQ ID NOS:6 and 49, SEQ ID NOS:7 and 50, SEQ ID NOS:3 and 44, SEQ ID NOS:3 and 45, SEQ ID NOS:3 and 47, SEQ ID NOS:3 and 48, SEQ ID NOS:3 and 49, SEQ ID NOS:3 and 50, SEQ ID NOS:7 and 44, SEQ ID NOS:7 and 45, SEQ ID NOS:7 and 47, SEQ ID NOS:7 and 48, SEQ ID NOS:8 and 51, SEQ ID NOS:9 and 52, SEQ ID NOS:10 and 53, SEQ ID NOS:11 and 54, SEQ ID NOS:12 and 55, SEQ ID NOS:13 and 56, SEQ ID NOS:14 and 57, SEQ ID NOS:15 and 58, SEQ ID NOS:16 and 59, SEQ ID NOS:17 and 60, SEQ ID NOS:18 and 61, SEQ ID NOS:19 and 62, SEQ ID NOS:20 and 63, SEQ ID NOS:21 and 64, SEQ ID NOS:22 and 65, SEQ ID NOS:23 and 66, SEQ ID NOS:24 and 67, SEQ ID NOS:25 and 68, SEQ ID NOS:26 and 69, SEQ ID NOS:27 and 70, SEQ ID NOS:28 and 71, SEQ ID NOS:29 and 72, SEQ ID NOS:30 and 73, SEQ ID NOS:31 and 74, SEQ ID NOS:32 and 75, SEQ ID NOS:33 and 76, SEQ ID NOS:34 and 77, SEQ ID NOS:35 and 78, SEQ ID NOS:36 and 79, SEQ ID NOS:37 and 80, SEQ ID NOS:38 and 81, SEQ ID NOS:39 and 82, SEQ ID NOS:40 and 83, SEQ ID NOS:41 and 84, SEQ ID NOS:42 and 85, SEQ ID NOS:43 and 86, SEQ ID NOS:3 and 48, SEQ ID NOS:360 and 48, SEQ ID NOS:3 and 365, SEQ ID NOS:16 and 59, SEQ ID NOS:18 and 61, SEQ ID NOS:34 and 77, SEQ ID NOS:34 and 379, SEQ ID NOS:18 and 376, SEQ ID NOS:18 and 377, and SEQ ID NOS:18 and 378.

64. A method of ameliorating symptoms of a disorder in which TIMP-1 is elevated, comprising the step of:

administering to a patient having the disorder an effective amount of a human antibody which neutralizes an MMP-inhibiting activity of the TIMP-1, whereby symptoms of the disorder are ameliorated.

65. The method of claim 64 wherein the MMP is human MMP-1.

66. The method of claim 64 wherein the MMP is rat MMP-13.

67. The method of claim 64 wherein the disorder is selected from the group consisting of liver fibrosis, alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus nephritis, glomerulosclerotic renal disease, idiopathic pulmonary fibrosis, benign prostate hypertrophy, lung cancer, and colon cancer.

68. The method of claim 64 wherein the antibody comprises a VHCDR3 and a VLCDR3 amino acid sequence pair selected from the group consisting of SEQ ID NOS:1 and 44, SEQ ID NOS:2 and 45, SEQ ID NO:3 and 46, SEQ ID NOS:4 and 47, SEQ ID NOS:5 and 48, SEQ ID NOS:6 and 49, SEQ ID NOS:7 and 50, SEQ ID NOS:3 and 44, SEQ ID NOS:3 and 45, SEQ ID NOS:3 and 47, SEQ ID NOS:3 and 48, SEQ ID NOS:3 and 49, SEQ ID NOS:3 and 50, SEQ ID NOS:7 and 44, SEQ ID NOS:7 and 45, SEQ ID NOS:7 and 47, SEQ ID NOS:7 and 48, SEQ ID NOS:8 and 51, SEQ ID NOS:9 and 52, SEQ ID NOS:10 and 53, SEQ ID NOS:11 and 54, SEQ ID NOS:12 and 55, SEQ ID NOS:13 and 56, SEQ ID NOS:14 and 57, SEQ ID NOS:15 and 58, SEQ ID NOS:16 and 59, SEQ ID NOS:17 and 60, SEQ ID NOS:18 and 61, SEQ ID NOS:19 and 62, SEQ ID NOS:20 and 63, SEQ ID NOS:21 and 64, SEQ ID NOS:22 and 65, SEQ ID NOS:23 and 66, SEQ ID NOS:24 and 67, SEQ ID NOS:25 and 68, SEQ ID NOS:26 and 69, SEQ ID NOS:27 and 70, SEQ ID NOS:28 and 71,

SEQ ID NOS:29 and 72, SEQ ID NOS:30 and 73, SEQ ID NOS:31 and 74, SEQ ID NOS:32 and 75, SEQ ID NOS:33 and 76, SEQ ID NOS:34 and 77, SEQ ID NOS:35 and 78, SEQ ID NOS:36 and 79, SEQ ID NOS:37 and 80, SEQ ID NOS:38 and 81, SEQ ID NOS:39 and 82, SEQ ID NOS:40 and 83, SEQ ID NOS:41 and 84, SEQ ID NOS:42 and 85, SEQ ID NOS:43 and 86, SEQ ID NOS:3 and 48, SEQ ID NOS:360 and 48, SEQ ID NOS:3 and 365, SEQ ID NOS:16 and 59, SEQ ID NOS:18 and 61, SEQ ID NOS:34 and 77, SEQ ID NOS:34 and 379, SEQ ID NOS:18 and 376, SEQ ID NOS:18 and 377, and SEQ ID NOS:18 and 378.

69. A method of detecting a TIMP-1 in a test preparation, comprising the steps of:
 - contacting the test preparation with a human antibody that specifically binds to the TIMP-1; and
 - assaying the test preparation for the presence of an antibody-TIMP-1 complex.
70. The method of claim 69 wherein the antibody comprises a detectable label.
71. The method of claim 69 wherein the antibody is bound to a solid support.
72. The method of claim 69 wherein the antibody comprises a VHCDR3 and a VLCDR3 amino acid sequence pair selected from the group consisting of SEQ ID NOS:1 and 44, SEQ ID NOS:2 and 45, SEQ ID NO:3 and 46, SEQ ID NOS:4 and 47, SEQ ID NOS:5 and 48, SEQ ID NOS:6 and 49, SEQ ID NOS:7 and 50, SEQ ID NOS:3 and 44, SEQ ID NOS:3 and 45, SEQ ID NOS:3 and 47, SEQ ID NOS:3 and 48, SEQ ID NOS:3 and 49, SEQ ID NOS:3 and 50, SEQ ID NOS:7 and 44, SEQ ID NOS:7 and 45, SEQ ID NOS:7 and 47, SEQ ID NOS:7 and 48, SEQ ID NOS:8 and 51, SEQ ID NOS:9 and 52, SEQ ID NOS:10 and 53, SEQ ID NOS:11 and 54, SEQ ID NOS:12 and 55, SEQ ID NOS:13 and 56, SEQ ID

NOS:14 and 57, SEQ ID NOS:15 and 58, SEQ ID NOS:16 and 59, SEQ ID NOS:17 and 60, SEQ ID NOS:18 and 61, SEQ ID NOS:19 and 62, SEQ ID NOS:20 and 63, SEQ ID NOS:21 and 64, SEQ ID NOS:22 and 65, SEQ ID NOS:23 and 66, SEQ ID NOS:24 and 67, SEQ ID NOS:25 and 68, SEQ ID NOS:26 and 69, SEQ ID NOS:27 and 70, SEQ ID NOS:28 and 71, SEQ ID NOS:29 and 72, SEQ ID NOS:30 and 73, SEQ ID NOS:31 and 74, SEQ ID NOS:32 and 75, SEQ ID NOS:33 and 76, SEQ ID NOS:34 and 77, SEQ ID NOS:35 and 78, SEQ ID NOS:36 and 79, SEQ ID NOS:37 and 80, SEQ ID NOS:38 and 81, SEQ ID NOS:39 and 82, SEQ ID NOS:40 and 83, SEQ ID NOS:41 and 84, SEQ ID NOS:42 and 85, and SEQ ID NOS:43 and 86.

73. A method to aid in diagnosing a disorder in which a TIMP-1 level is elevated, comprising the steps of:

contacting a sample from a patient suspected of having the disorder with a human antibody that binds to TIMP-1; and

assaying for the presence of an antibody-TIMP-1 complex, whereby detection of an amount of the complex which is greater than an amount of the complex in a normal sample identifies the patient as likely to have the disorder.

74. The method of claim 73 wherein the antibody comprises a detectable label.

75. The method of claim 73 wherein the antibody is bound to a solid support.

76. The method of claim 73 wherein the antibody comprises a VHCDR3 and a VLCDR3 amino acid sequence pair selected from the group consisting of SEQ ID NOS:1 and 44, SEQ ID NOS:2 and 45, SEQ ID NO:3 and 46, SEQ ID NOS:4 and 47, SEQ ID

NOS:5 and 48, SEQ ID NOS:6 and 49, SEQ ID NOS:7 and 50, SEQ ID NOS:3 and 44, SEQ ID NOS:3 and 45, SEQ ID NOS:3 and 47, SEQ ID NOS:3 and 48, SEQ ID NOS:3 and 49, SEQ ID NOS:3 and 50, SEQ ID NOS:7 and 44, SEQ ID NOS:7 and 45, SEQ ID NOS:7 and 47, SEQ ID NOS:7 and 48, SEQ ID NOS:8 and 51, SEQ ID NOS:9 and 52, SEQ ID NOS:10 and 53, SEQ ID NOS:11 and 54, SEQ ID NOS:12 and 55, SEQ ID NOS:13 and 56, SEQ ID NOS:14 and 57, SEQ ID NOS:15 and 58, SEQ ID NOS:16 and 59, SEQ ID NOS:17 and 60, SEQ ID NOS:18 and 61, SEQ ID NOS:19 and 62, SEQ ID NOS:20 and 63, SEQ ID NOS:21 and 64, SEQ ID NOS:22 and 65, SEQ ID NOS:23 and 66, SEQ ID NOS:24 and 67, SEQ ID NOS:25 and 68, SEQ ID NOS:26 and 69, SEQ ID NOS:27 and 70, SEQ ID NOS:28 and 71, SEQ ID NOS:29 and 72, SEQ ID NOS:30 and 73, SEQ ID NOS:31 and 74, SEQ ID NOS:32 and 75, SEQ ID NOS:33 and 76, SEQ ID NOS:34 and 77, SEQ ID NOS:35 and 78, SEQ ID NOS:36 and 79, SEQ ID NOS:37 and 80, SEQ ID NOS:38 and 81, SEQ ID NOS:39 and 82, SEQ ID NOS:40 and 83, SEQ ID NOS:41 and 84, SEQ ID NOS:42 and 85, SEQ ID NOS:43 and 86, SEQ ID NOS:3 and 48, SEQ ID NOS:360 and 48, SEQ ID NOS:3 and 365, SEQ ID NOS:16 and 59, SEQ ID NOS:18 and 61, SEQ ID NOS:34 and 77, SEQ ID NOS:34 and 379, SEQ ID NOS:18 and 376, SEQ ID NOS:18 and 377, and SEQ ID NOS:18 and 378.

77. The method of claim 73 wherein the sample is obtained from a tissue selected from the group consisting of colon, liver, heart, kidney, prostate, serum, and lung.

78. The method of claim 73 wherein the disorder is selected from the group consisting of liver fibrosis, alcoholic liver disease, cardiac fibrosis, acute cardiac syndrome,

lupus nephritis, glomerulosclerotic renal disease, benign prostate hypertrophy, lung cancer, colon cancer, and idiopathic pulmonary fibrosis.

Sequence Summary HucAL Libraries scFv1, scFv2, scFv3 and Fab1

VL

Position	Framework 1												Framework 2													
	CDR 3												CDR 3													
1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	6	
Ec01V	D	I	Q	M	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T	T	C	N	S	S	A
BamII																										
VLk1	D	I	V	M	T	Q	S	P	L	S	L	P	V	T	P	G	E	P	A	S	S	C	N	N	A	
VLk2	D	I	V	L	T	Q	S	P	A	T	L	S	L	S	P	G	E	P	A	S	S	C	N	N	A	
VLk3	D	I	V	L	T	Q	S	P	A	T	L	S	L	S	P	G	E	P	A	S	S	C	N	N	A	
VLk4	D	I	V	M	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	N	C	S	S	A	
PstI																										
VLJ1	D	I	V	L	T	Q	P	P	-	S	V	S	G	A	P	G	Q	R	V	T	I	S	C	S	S	A
VLJ2	D	I	A	L	T	Q	P	A	-	S	V	S	G	S	P	G	Q	S	I	T	I	S	C	S	S	A
VLJ3	D	I	E	L	T	Q	P	P	-	S	V	S	V	A	P	G	Q	T	A	R	I	S	C	S	S	A
Ec01V																										
BSS1																										

VH

Position	Framework 1												Framework 2															
	CDR 1												CDR 1															
1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	6	7	8	
MfEl																												
VH1A	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V	S	C	K	A	S	G	C	
VH1B	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V	S	C	K	A	S	G	C	
VH2	Q	V	Q	L	K	E	S	G	P	A	L	V	K	P	T	Q	T	L	T	C	F	S	G	T	S	T	S	
VH3	Q	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L	S	C	A	S	G	T	S	
VH4	Q	V	Q	L	Q	E	S	G	P	G	L	V	K	P	S	E	T	L	S	L	T	C	V	S	G	T	S	
VH5	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	E	S	L	K	I	S	C	K	G	S	G	T	S
VH6	Q	V	Q	L	Q	Q	S	G	P	G	L	V	K	P	S	Q	T	L	S	L	T	C	A	I	S	G	T	S

F16.1

Framework 2		CDR 2		Framework 3	
4	5	6	7	8	9
5	6	7	8	9	0
6	7	8	9	0	1
7	8	9	0	1	2
8	9	0	1	2	3
9	0	1	2	3	4
5	6	7	8	9	0
6	7	8	9	0	1
7	8	9	0	1	2
8	9	0	1	2	3
9	0	1	2	3	4

Framework 2		CDR 2		Framework 3	
4	5	6	7	8	9
5	6	7	8	9	0
6	7	8	9	0	1
7	8	9	0	1	2
8	9	0	1	2	3
9	0	1	2	3	4

Framework 2		CDR 2		Framework 3	
4	5	6	7	8	9
5	6	7	8	9	0
6	7	8	9	0	1
7	8	9	0	1	2
8	9	0	1	2	3
9	0	1	2	3	4

Fig. 1, cont.

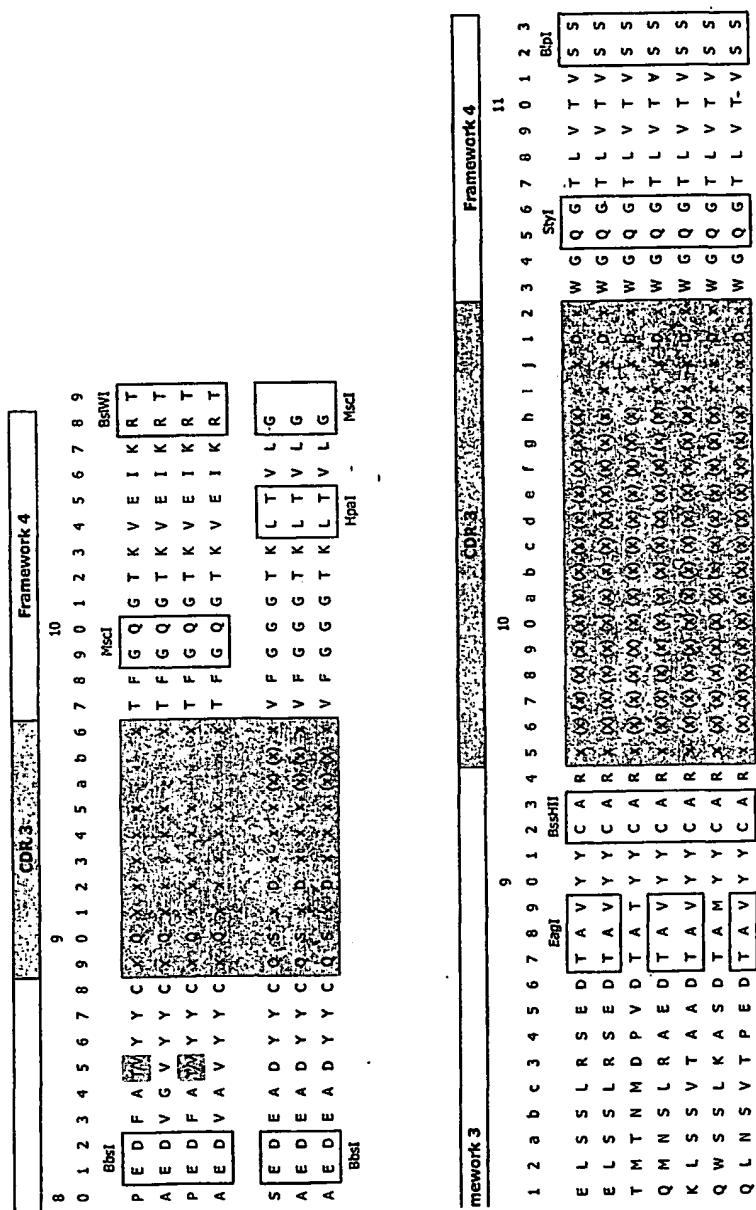


Fig. 1, cont.

Sequence Summary HuCAL Libraries scFv1, scFv2, scFv3 and Fab1

VL

Position	Framework 1								Framework 2								Framework 3											
	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	6	7	8
EcERV	BamH1	GAT	ATC	CAG	ATG	ACC	CAG	CGG	AGC	GTC	GCT	GAT	GTC	ACC	GCT	GCG	GTC	ATG	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT
VLx1		GAT	ATC	CAG	ATG	ACC	CAG	CGG	AGC	GTC	GCT	GAT	GTC	ACC	GCT	GCG	GTC	ATG	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT
VLx2		GAT	ATC	CAG	ATG	ACC	CAG	CGG	AGC	GTC	GCT	GAT	GTC	ACC	GCT	GCG	GTC	ATG	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT
VLx3		GAT	ATC	CAG	ATG	ACC	CAG	CGG	AGC	GTC	GCT	GAT	GTC	ACC	GCT	GCG	GTC	ATG	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT
VLx4		GAT	ATC	CAG	ATG	ACC	CAG	CGG	AGC	GTC	GCT	GAT	GTC	ACC	GCT	GCG	GTC	ATG	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT
EcERV	BamH1	GAT	ATC	CAG	ATG	ACC	CAG	CGG	AGC	GTC	GCT	GAT	GTC	ACC	GCT	GCG	GTC	ATG	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT
VLx1		GAT	ATC	CAG	ATG	ACC	CAG	CGG	AGC	GTC	GCT	GAT	GTC	ACC	GCT	GCG	GTC	ATG	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT
VLx2		GAT	ATC	CAG	ATG	ACC	CAG	CGG	AGC	GTC	GCT	GAT	GTC	ACC	GCT	GCG	GTC	ATG	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT
VLx3		GAT	ATC	CAG	ATG	ACC	CAG	CGG	AGC	GTC	GCT	GAT	GTC	ACC	GCT	GCG	GTC	ATG	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT
VLx4		GAT	ATC	CAG	ATG	ACC	CAG	CGG	AGC	GTC	GCT	GAT	GTC	ACC	GCT	GCG	GTC	ATG	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT
EcERV	BamH1	GAT	ATC	CAG	ATG	ACC	CAG	CGG	AGC	GTC	GCT	GAT	GTC	ACC	GCT	GCG	GTC	ATG	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT

VH

Position	Framework 1								Framework 2								Framework 3												
	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	6	7	8	
VH1A	MfeI	GAT	CAA	TTC	GTC	GCG	GAA	GTC	AAA	AAA	CCC	GGC	AGC	GTC	AAA	GTC	AGC	GTC	AAA	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT
VH1B		GAT	CAA	TTC	GTC	GCG	GAA	GTC	AAA	AAA	CCC	GGC	AGC	GTC	AAA	GTC	AGC	GTC	AAA	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT
VH2		GAT	CAA	TTC	GTC	GCG	GAA	GTC	AAA	AAA	CCC	GGC	AGC	GTC	AAA	GTC	AGC	GTC	AAA	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT
VH3		GAT	CAA	TTC	GTC	GCG	GAA	GTC	AAA	AAA	CCC	GGC	AGC	GTC	AAA	GTC	AGC	GTC	AAA	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT
VH4		GAT	CAA	TTC	GTC	GCG	GAA	GTC	AAA	AAA	CCC	GGC	AGC	GTC	AAA	GTC	AGC	GTC	AAA	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT
VH5		GAT	CAA	TTC	GTC	GCG	GAA	GTC	AAA	AAA	CCC	GGC	AGC	GTC	AAA	GTC	AGC	GTC	AAA	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT
VH6		GAT	CAA	TTC	GTC	GCG	GAA	GTC	AAA	AAA	CCC	GGC	AGC	GTC	AAA	GTC	AGC	GTC	AAA	GTC	ATG	TAT	TCT	TAT	TCT	TAT	TCT	TAT	TCT

Fig.2

Work 2		Work 3									
		Core					Ext.				
Xtal	Xtal	Base II					Base III				
		5	6	7	8	9	0	1	2	3	4
CAG	GTC	TGG	ATG	GCC	GGC	ATT	ATT	CGC	ATT	TTC	CGC
CAG	GTC	TGG	ATG	GCC	GGC	TGG	ATT	AAC	CGC	ATT	CGC
AAA	GCC	CTC	GAG	TGG	GCT	CGT	ATT	GAT	TAT	ATG	GAT
AAG	GGT	CTC	GAG	TGG	GCT	GCT	ATT	GAT	TAT	ATG	GAT
AAG	GGT	CTC	GAG	TGG	GCT	GCT	ATT	GAT	TAT	ATG	GAT
CCT	GCC	CTC	GAG	TGG	GCT	GCT	ATT	GAT	TAT	ATG	GAT
CAG	GTC	TGG	ATG	GCC	GGC	ATT	ATT	CGC	ATT	TTC	CGC
CAG	GTC	TGG	ATG	GCC	GGC	TGG	ATT	AAC	CGC	ATT	CGC
AAA	GCC	CTC	GAG	TGG	GCT	CGT	ATT	GAT	TAT	ATG	GAT
AAG	GGT	CTC	GAG	TGG	GCT	GCT	ATT	GAT	TAT	ATG	GAT
AAG	GGT	CTC	GAG	TGG	GCT	GCT	ATT	GAT	TAT	ATG	GAT
CCT	GCC	CTC	GAG	TGG	GCT	GCT	ATT	GAT	TAT	ATG	GAT
NspV											
3	4	5	6	7	8	9	0	1	2	3	4
5	6	7	8	9	0	1	2	3	4	5	6
7	8	9	0	1	2	3	4	5	6	7	8
8	9	0	1	2	3	4	5	6	7	8	9
0	1	2	3	4	5	6	7	8	9	0	1
1	2	3	4	5	6	7	8	9	0	1	2
2	3	4	5	6	7	8	9	0	1	2	3
3	4	5	6	7	8	9	0	1	2	3	4
4	5	6	7	8	9	0	1	2	3	4	5
5	6	7	8	9	0	1	2	3	4	5	6
6	7	8	9	0	1	2	3	4	5	6	7
7	8	9	0	1	2	3	4	5	6	7	8
8	9	0	1	2	3	4	5	6	7	8	9
9	0	1	2	3	4	5	6	7	8	9	0

FIG. 2, cont.

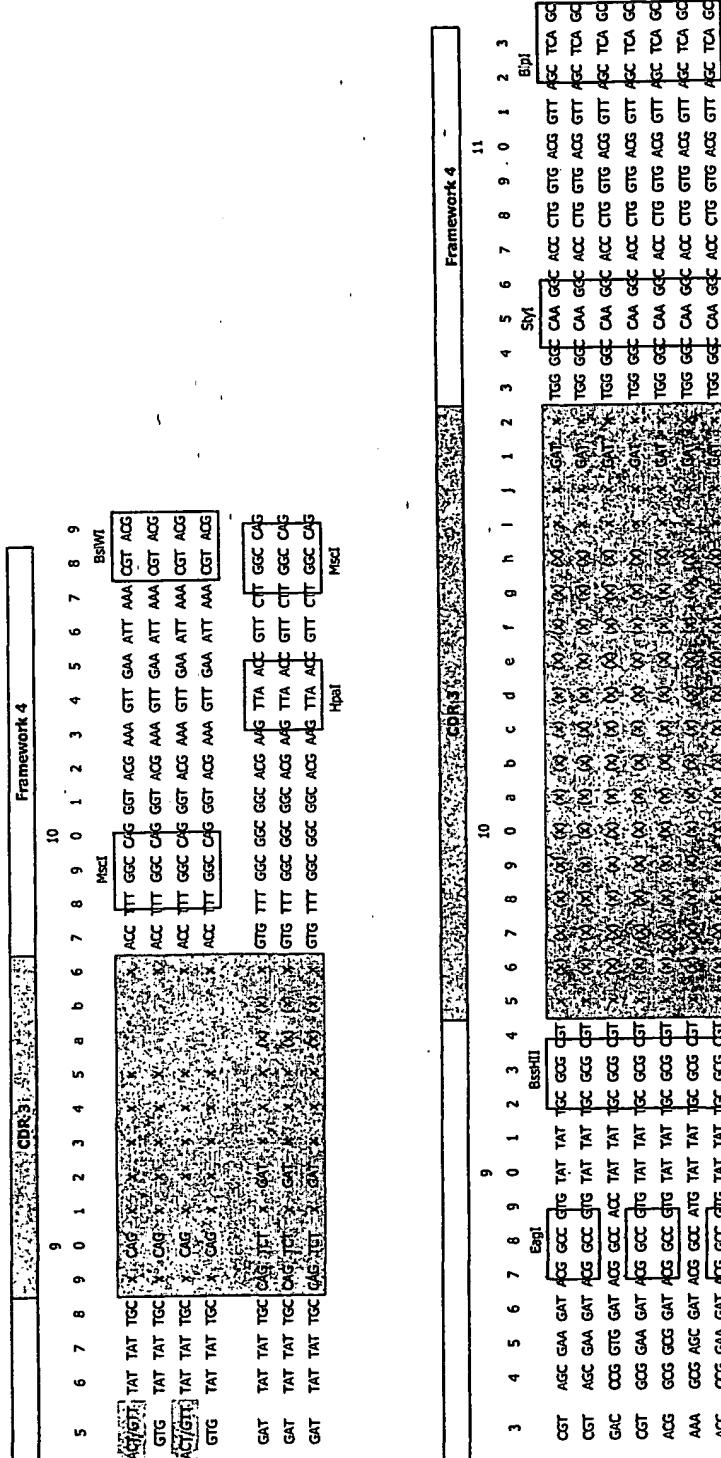


Fig. 2, cont.

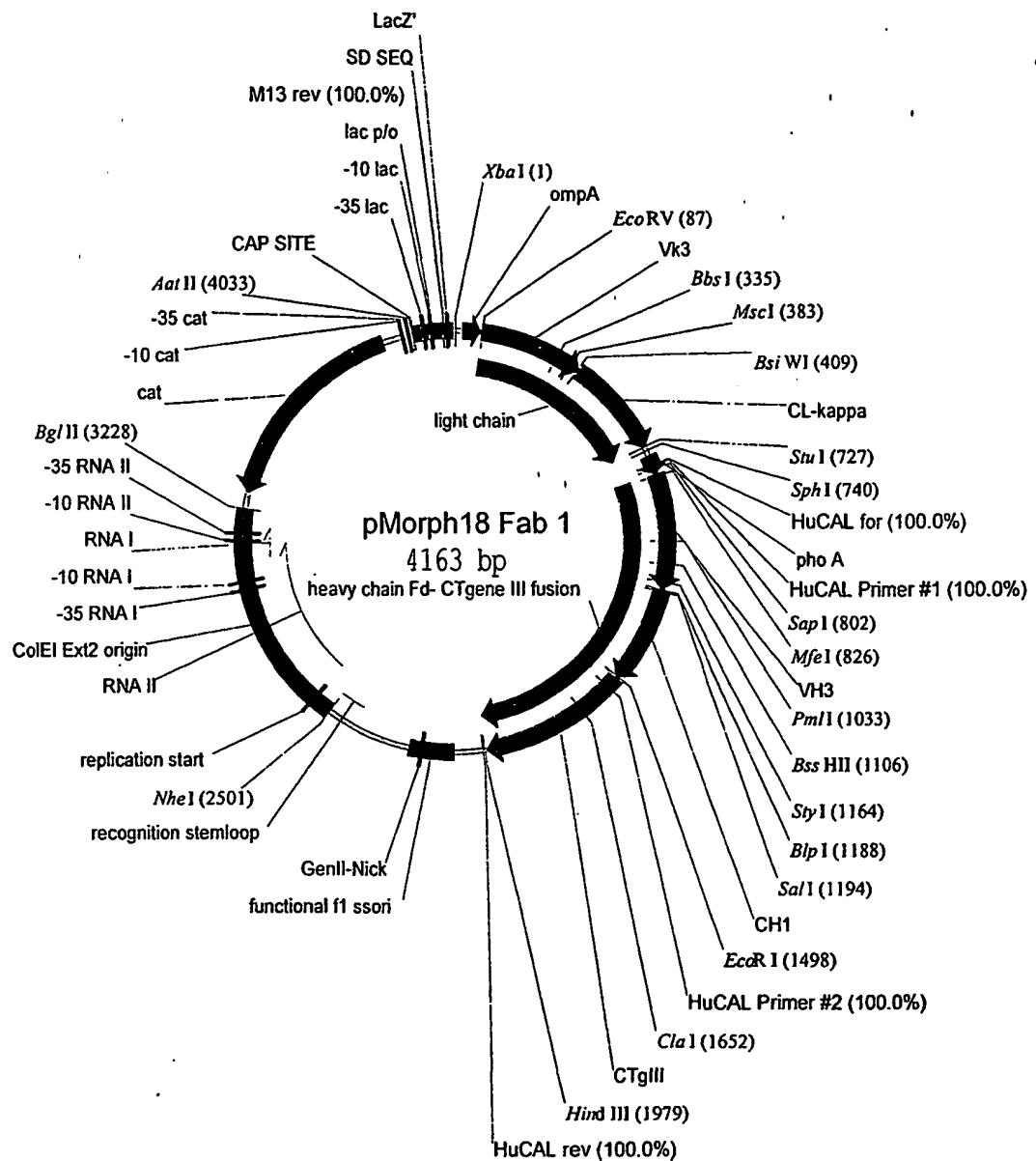


FIG. 3

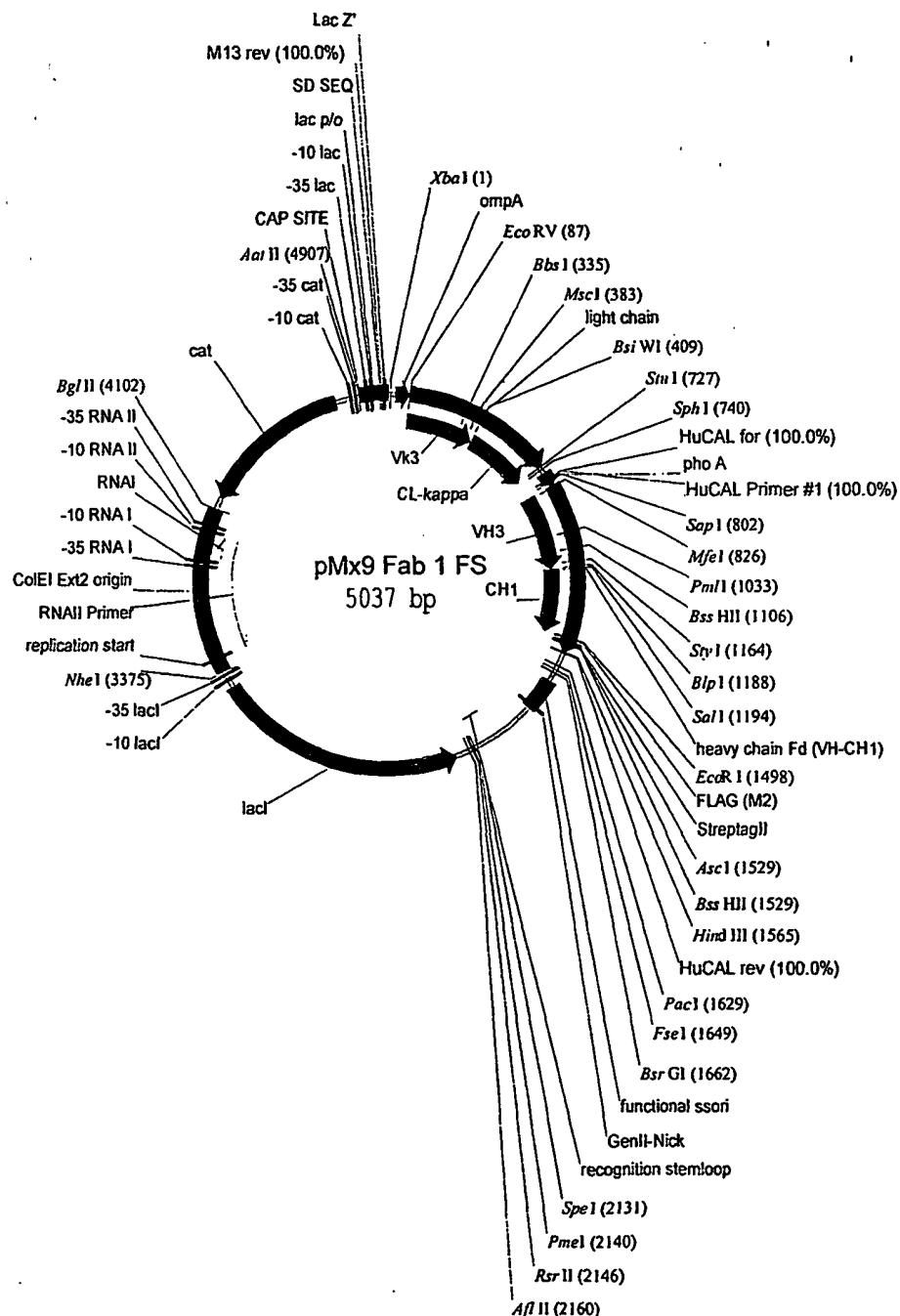


FIG. 4

FIG. 5

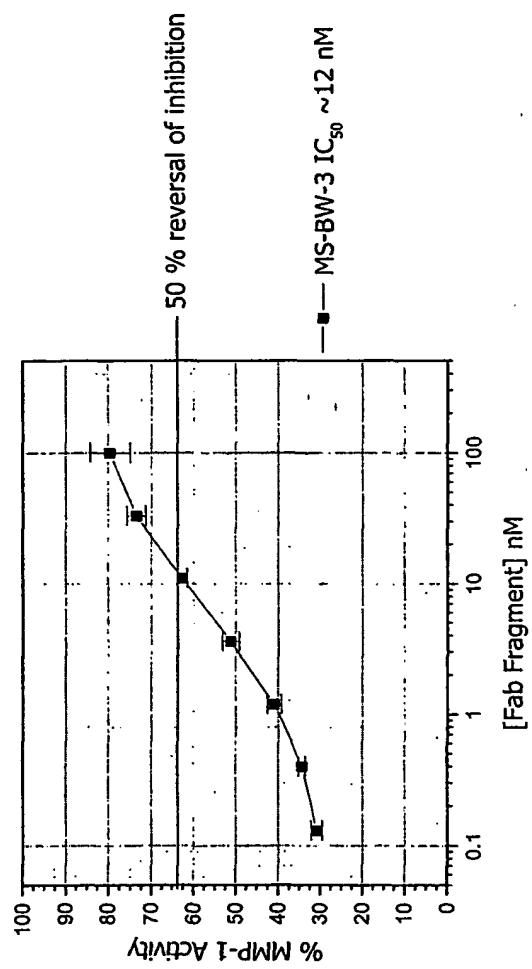


FIG. 6

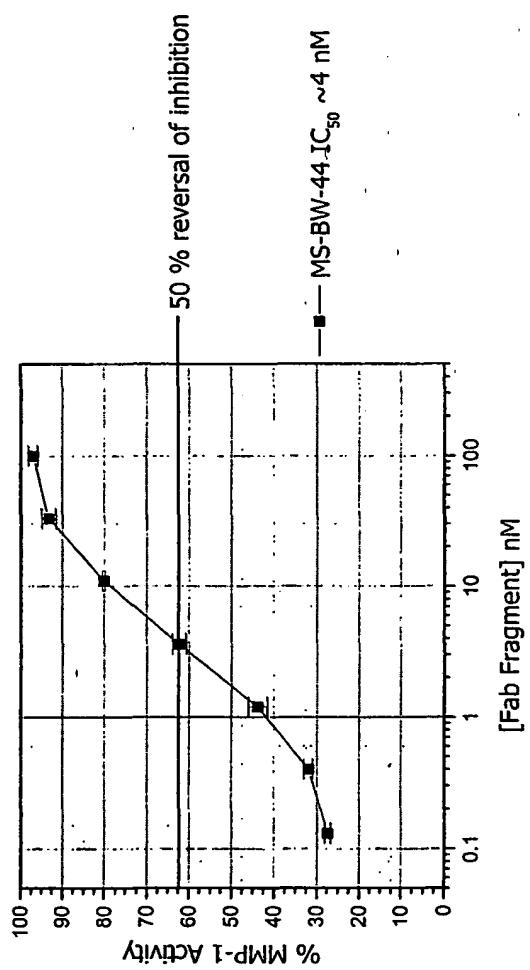


FIG. 7

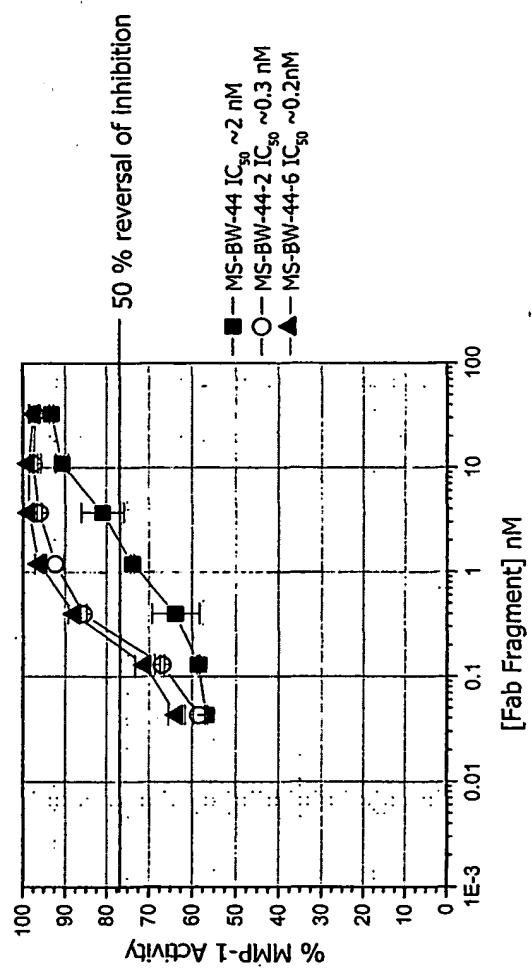


FIG. 8

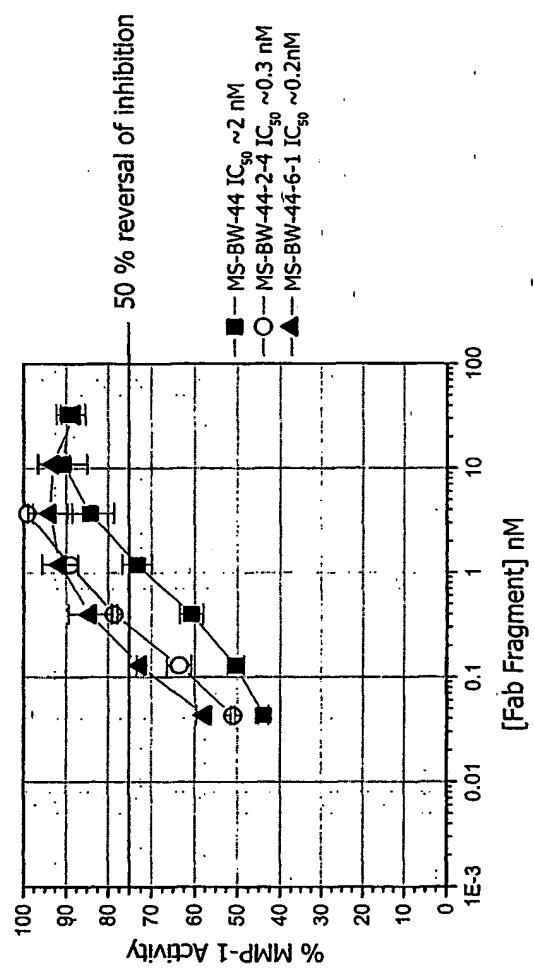


FIG. 9

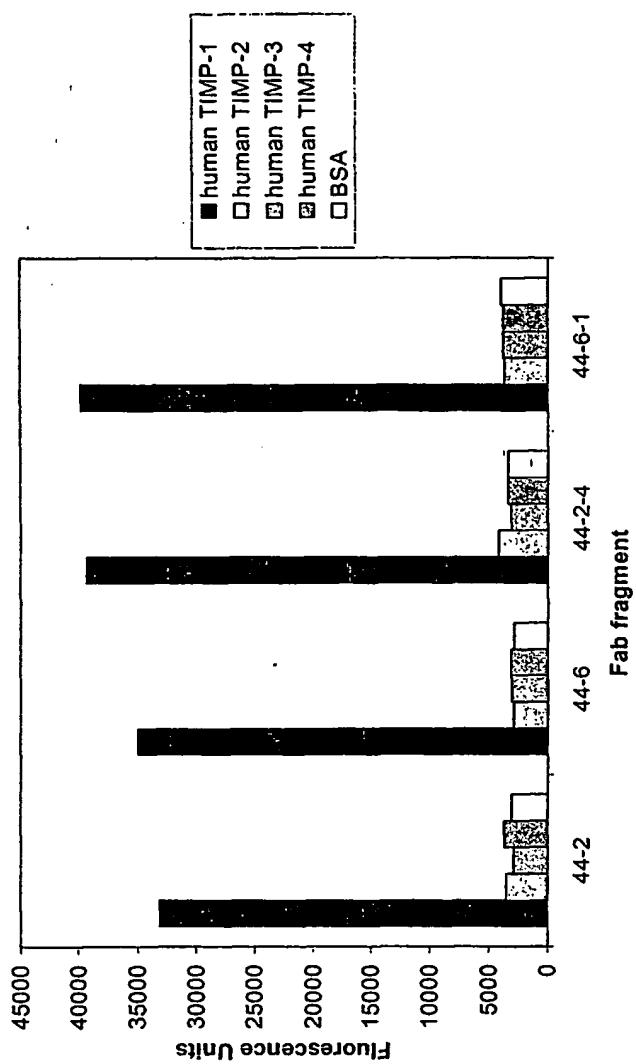


FIG. 10

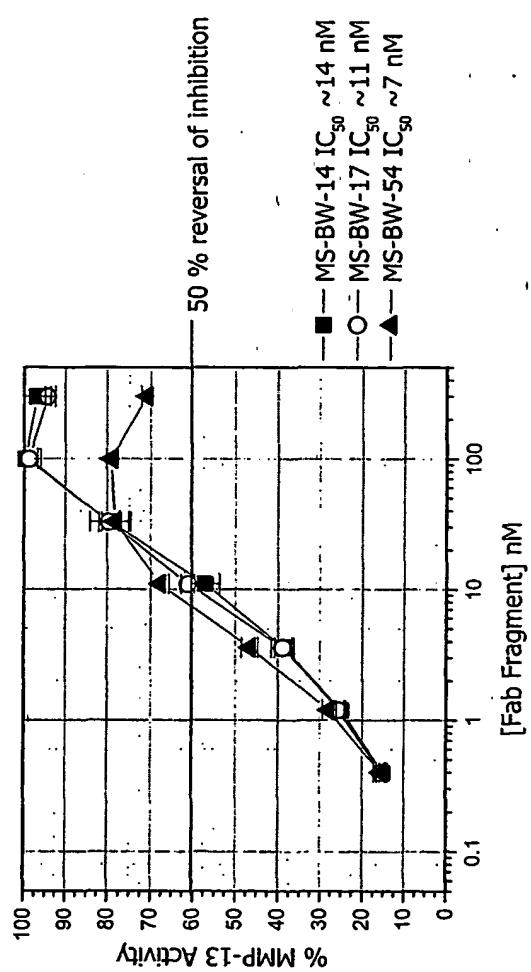


FIG. 11

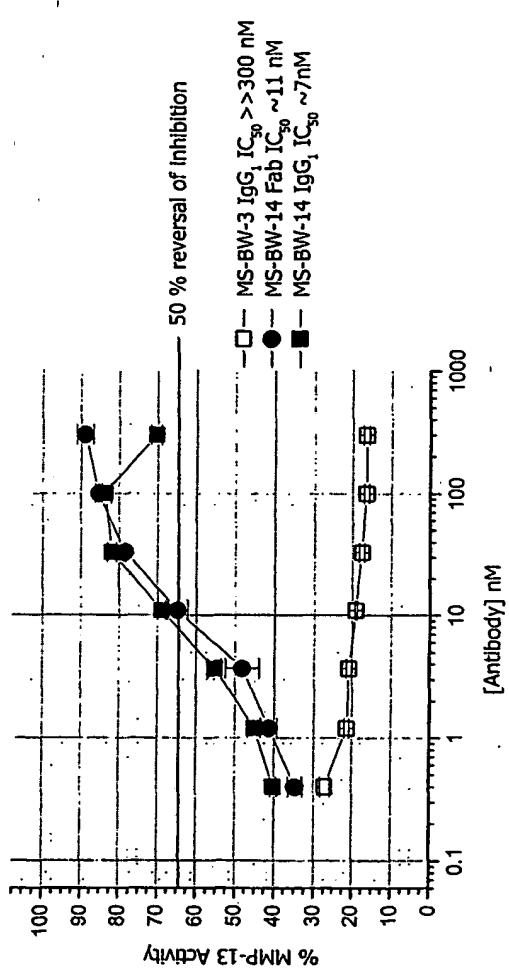


FIG. 12

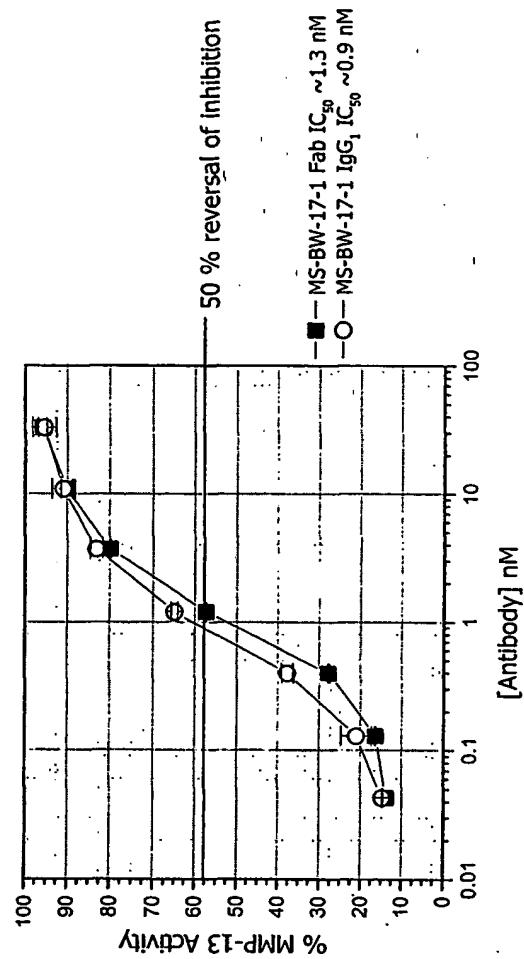


FIG. 13

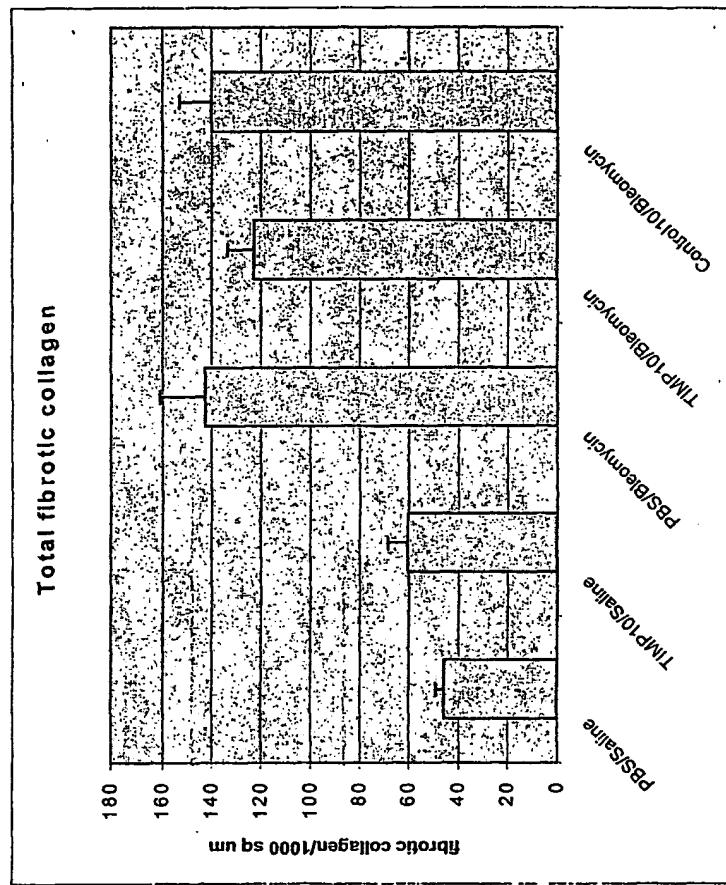
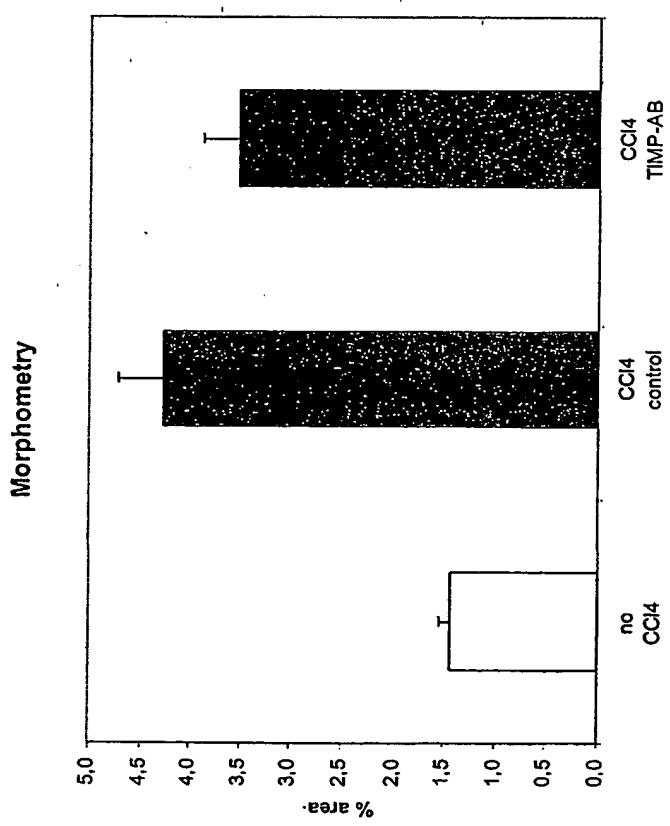


FIG. 14

FIG. 15



SEQUENCE LISTING

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Trp Met Thr Pro Pro Gly His Tyr Tyr Gly Tyr Thr Phe Asp Val
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<400> 39
Leu Arg Val His Asp Tyr Ala Met Tyr Phe Asp Leu
1 5 10

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Phe Val Ser Tyr Asn Gly Ser Val Pro Tyr Phe Asp Tyr
1 5 10

<210> 41
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<400> 41
Ile Ile Gly Asp Tyr Val Ile Phe Phe Asp Val
1 5 10

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<400> 42
Leu Phe Thr Tyr Pro Phe Leu Tyr Phe Asp Val
1 5 10

<210> 43
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<400> 43
Ile Leu Thr Gly His Val Leu Leu Phe Asp Tyr
1 5 10

<210> 44
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<400> 44
Gln Ser Tyr Asp Tyr Gln Gln Phe Thr
1 5

<210> 45
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<400> 45
Gln Ser Tyr Asp Phe Lys Thr Tyr Leu
1 5

<210> 46
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<400> 46
Gln Ser Tyr Asp Phe Leu Arg Phe Ser
1 5

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<400> 47
Gln Ser Tyr Asp Phe Ile Asn Val Ile
1 5

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Gln Ser Tyr Asp Phe Val Arg Phe Met
1 5

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Gln Ser Tyr Asp Phe Tyr Lys Phe Asn
1 5

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Gln Ser Tyr Asp Phe Arg Arg Phe Ser
1 5

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Gln Ser Arg Asp Phe Asn Arg Gly Pro
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Gln Ser Tyr Asp Gln Arg Lys Trp
1 5

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Gln Gln Leu Tyr Gly Thr Val Ser
1 5

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<400> 54
Gln Ser Tyr Asp Gly Phe Lys Thr His
1 5

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<400> 55
Gln Ser Tyr Asp Tyr Ser Leu Leu
1 5

<210> 56
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<400> 56
Gln Ser Tyr Asp Phe Asn Phe His
1 5

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Gln Ser Tyr Asp Met Ile Ala Arg Tyr Pro
1 5 10

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<400> 58
Gln Ser Trp Asp Ile His Pro Phe Asp Val
1 5 10

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Gln Ser Trp Asp Leu Glu Pro Tyr
1 5

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Gln Ser Tyr Asp Val Leu Asp Ser Glu
1 5

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<400> 61
Gln Ser Tyr Asp Pro Ser His Pro Ser Lys
1 5 10

<210> 62
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<400> 62
Gln Ser Tyr Asp Asp Met Gln Phe
1 5

<210> 63
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<400> 63
Gln Ser Trp Asp Ile Asn His Ala Ile
1 5

<210> 64
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<400> 64

Gln Ser Tyr Asp Tyr Tyr Asp Tyr Gly
1 5

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Gln Gln Ala Asn Asp Phe Pro Ile
1 5

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Gln Ser Trp Asp Asn Leu Lys Met Pro Val
1 5 10

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<400> 67
Gln Ser Tyr Asp Val Phe Pro Ile Asn Arg
1 5 10

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Gln Ser Asp Leu Tyr Phe Pro
1 5

<210> 69
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<400> 69
Gln Ser Tyr Asp Val Thr Pro Arg
1 5

<210> 70
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<400> 70
Gln Ser Tyr Asp Pro Val Gly Phe Pro
1 5

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<400> 71
Gln Ser Tyr Asp Leu Ser Pro Arg
1 5

<210> 72
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<400> 72
Gln Ser Tyr Asp Phe Ser His Tyr Phe Phe
1 5 10

<210> 73
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<400> 73
Gln Ser Tyr Asp Leu Arg Tyr Ser His
1 5

<210> 74
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<400> 74
Gln Ser Tyr Asp Leu Arg Asn Arg
1 5

<210> 75
<211> 9
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<400> 75
Gln Ser Tyr Asp Phe Thr Tyr Gly Ser

1 5

<210> 76
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<400> 76
Gln Gln Phe Asn Asp Ser Pro Tyr
1 5

<210> 77
<211> 9
<212> PRT
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<400> 77
Gln Ser Tyr Asp Ile Ser Gly Tyr Pro
1 5

<210> 78
<211> 10
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<400> 78
Gln Ser Arg Asp Leu Tyr Tyr Val Tyr Tyr
1 5 10

<210> 79
<211> 8
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<400> 79
Gln Ser Tyr Asp Arg Ser Met Trp
1 5

<210> 80
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<400> 80
Gln Ser Trp Asp Val Gln Thr Asp Lys
1 5

<210> 81
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<400> 81
Gln Ser Trp Asp Pro Ser His Tyr Tyr
1 5

<210> 82
<211> 9
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<400> 82
Gln Ser Tyr Asp Ile Met Pro Glu Arg
1 5

<210> 83
<211> 9
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<400> 83
Gln Ser Met Asp Phe Arg Leu Met His
1 5

<210> 84
<211> 9
<212> PRT
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<400> 84
Gln Ser Phe Asp Met Ile His Pro Tyr
1 5

<210> 85
<211> 7
<212> PRT
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<400> 85
Gln Ser Asp Phe Pro Val Met
1 5

<210> 86
<211> 7
<212> PRT
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<400> 86
Gln Ser Asp Asn Pro Tyr Leu
1 5

<210> 87
<211> 11
<212> PRT
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<400> 87
Thr Cys Val Pro Pro His Pro Gln Thr Ala Phe
1 5 10

<210> 88
<211> 12
<212> PRT
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<400> 88
Cys Thr Ser Val Pro Pro His Pro Gln Thr Ala Phe
1 5 10

<210> 89
<211> 12
<212> PRT
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<400> 89
Ser Thr Cys Val Pro Pro His Pro Gln Thr Ala Phe
1 5 10

<210> 90
<211> 13
<212> PRT
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<400> 90
Ser Thr Ser Val Pro Pro His Pro Gln Thr Ala Phe Cys
1 5 10

<210> 91
<211> 10
<212> PRT
<213> Homo sapiens

<400> 91
Cys Glu Val Asn Gln Thr Thr Leu Tyr Gln
1 5 10

<210> 92
<211> 12
<212> PRT
<213> Homo sapiens

<400> 92
Pro Ala Met Glu Ser Val Cys Gly Tyr Phe His Arg
1 5 10

<210> 93
<211> 16
<212> PRT
<213> Homo sapiens

<400> 93
Pro Ala Met Glu Ser Val Cys Gly Tyr Phe His Arg Ser His Asn Arg
1 5 10 15

<210> 94
<211> 17
<212> PRT
<213> Homo sapiens

<400> 94
Cys Pro Ala Met Glu Ser Val Ser Gly Tyr Phe His Arg Ser His Asn
1 5 10 15
Arg

<210> 95
<211> 17
<212> PRT
<213> Homo sapiens

<400> 95
Pro Ala Met Glu Ser Val Ser Gly Tyr Phe His Arg Ser His Asn Arg
1 5 10 15
Cys

<210> 96
<211> 12
<212> PRT
<213> Homo sapiens

<400> 96
Cys Leu Trp Thr Asp Gln Leu Leu Gln Gly Ser Glu
1 5 10

<210> 97
<211> 215
<212> PRT
<213> Homo sapiens

<400> 97

Asp	Ile	Ala	Leu	'Thr	Gln	Pro	'Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln
1				5				10						15	
Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Gly	Tyr
				20				25					30		
Asn	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu
				35				40				45			
Met	Ile	Tyr	Asp	Val	Ser	Asn	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe
				50			55				60				
Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu
				65			70			75			80		
Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Tyr	Asp	Tyr	Gln
				85					90			95			
Gln	Phe	Thr	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln
				100				105				110			
Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	Glu	Glu
				115				120				125			
Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	Phe	Tyr
				130			135			140					
Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro	Val	Lys
				145			150			155			160		
Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	Lys	Tyr
				165				170			175				
Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	Ser	His
				180				185			190				
Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val	Glu	Lys
				195				200			205				
Thr	Val	Ala	Pro	Thr	Glu	Ala									
				210			215								

<210> 98

<211> 215

<212> PRT

<213> Homo sapiens

<400> 98

Asp	Ile	Ala	Leu	'Thr	Gln	Pro	'Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln
1				5				10					15		
Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Gly	Tyr
				20				25				30			
Asn	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu
				35				40			45				
Met	Ile	Tyr	Asp	Val	Ser	Asn	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe
				50			55			60					
Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu
				65			70			75			80		
Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Tyr	Asp	Phe	Lys
				85					90			95			
Thr	Tyr	Leu	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln
				100				105			110				

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
 115 120 125
 Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
 130 135 140
 Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
 145 150 155 160
 Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
 165 170 175
 Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
 180 185 190
 Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
 195 200 205
 Thr Val Ala Pro Thr Glu Ala
 210 215

<210> 99
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 99
 Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Leu
 85 90 95
 Arg Phe Ser Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110
 Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
 115 120 125
 Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
 130 135 140
 Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
 145 150 155 160
 Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
 165 170 175
 Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
 180 185 190
 Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
 195 200 205
 Thr Val Ala
 210

<210> 100
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 100
 Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Ile
 85 90 95
 Asn Val Ile Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110
 Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
 115 120 125
 Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
 130 135 140
 Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
 145 150 155 160
 Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
 165 170 175
 Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
 180 185 190
 Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
 195 200 205
 Thr Val Ala Pro Thr Glu Ala
 210 215

<210> 101
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 101
 Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu

65	70	75	80
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Val			
85	90	95	
Arg Phe Met Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln			
100	105	110	
Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu			
115	120	125	
Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr			
130	135	140	
Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys			
145	150	155	160
Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr			
165	170	175	
Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His			
180	185	190	
Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys			
195	200	205	
Thr Val Ala Pro Thr Glu Ala			
210	215		

<210> 102

<211> 215

<212> PRT

<213> Homo sapiens

<400> 102

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln			
1	5	10	15
Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr			
20	25	30	
Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu			
35	40	45	
Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe			
50	55	60	
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu			
65	70	75	80
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Tyr			
85	90	95	
Lys Phe Asn Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln			
100	105	110	
Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu			
115	120	125	
Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr			
130	135	140	
Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys			
145	150	155	160
Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr			
165	170	175	
Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His			
180	185	190	

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
 195 200 205
 Thr Val Ala Pro Thr Glu Ala
 210 215

<210> 103

<211> 215

<212> PRT

<213> Homo sapiens

<400> 103

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Arg
 85 90 95
 Arg Phe Ser Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110
 Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
 115 120 125
 Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
 130 135 140
 Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
 145 150 155 160
 Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
 165 170 175
 Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
 180 185 190
 Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
 195 200 205
 Thr Val Ala Pro Thr Glu Ala
 210 215

<210> 104

<211> 214

<212> PRT

<213> Homo sapiens

<400> 104

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
 1 5 10 15
 Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
 20 25 30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
 35 40 45
 Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
 65 70 75 80
 Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Arg Asp Phe Asn Arg
 85 90 95
 Gly Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 100 105 110
 Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
 115 120 125
 Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
 130 135 140
 Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala
 145 150 155 160
 Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala
 165 170 175
 Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
 180 185 190
 Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
 195 200 205
 Val Ala Pro Thr Glu Ala
 210

<210> 105

<211> 213

<212> PRT

<213> Homo sapiens

<400> 105
 Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln
 1 5 10 15
 Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
 20 25 30
 Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
 35 40 45
 Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
 50 55 60
 Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
 65 70 75 80
 Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Gln Arg Lys
 85 90 95
 Trp Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys
 100 105 110
 Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
 115 120 125
 Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
 130 135 140
 Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly

145	150	155	160
Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala			
165	170	175	
Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser			
180	185	190	
Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val			
195	200	205	
Ala Pro Thr Glu Ala			
210			

<210> 106

<211> 215

<212> PRT

<213> Homo sapiens

<400> 106

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly			
1	5	10	15
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser			
20	25	30	
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu			
35	40	45	
Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser			
50	55	60	
Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu			
65	70	75	80
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Tyr Gly Thr Ser			
85	90	95	
Val Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala			
100	105	110	
Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser			
115	120	125	
Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu			
130	135	140	
Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser			
145	150	155	160
Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu			
165	170	175	
Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val			
180	185	190	
Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys			
195	200	205	
Ser Phe Asn Arg Gly Glu Ala			
210	215		

<210> 107

<211> 214

<212> PRT

<213> Homo sapiens

<400> 107

Asp	Ile	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Gly	Ala	Pro	Gly	Gln
1						5			10				15		
Arg	Val	Thr	Ile	Ser	Cys	Ser	Gly	Ser	Ser	Ser	Asn	Ile	Gly	Ser	Asn
							20		25				30		
Tyr	Val	Ser	Trp	Tyr	Gln	Gln	Leu	Pro	Gly	Thr	Ala	Pro	Lys	Leu	Leu
							35		40			45			
Ile	Tyr	Asp	Asn	Asn	Gln	Arg	Pro	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser
						50		55			60				
Gly	Ser	Lys	Ser	Gly	Thr	Ser	Ala	Ser	Leu	Ala	Ile	Thr	Gly	Leu	Gln
						65		70			75		80		
Ser	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Tyr	Asp	Gly	Phe	Lys
						85			90			95			
Thr	His	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	Pro
						100			105			110			
Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	Glu	Glu	Leu
						115			120			125			
Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	Phe	Tyr	Pro
						130		135			140				
Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro	Val	Lys	Ala
						145		150			155		160		
Gly	Val	Glu	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	Lys	Tyr	Ala	
						165			170			175			
Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	Ser	His	Arg
						180			185			190			
Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val	Glu	Lys	Thr
						195			200			205			
Val	Ala	Pro	Thr	Glu	Ala										
						210									

<210> 108

<211> 211

<212> PRT

<213> Homo sapiens

<400> 108

Asp	Ile	Glu	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	Ala	Pro	Gly	Gln
1						5			10			15			
Thr	Ala	Arg	Ile	Ser	Cys	Ser	Gly	Asp	Ala	Leu	Gly	Asp	Lys	Tyr	Ala
						20			25			30			
Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	Ile	Tyr
						35		40			45				
Asp	Asp	Ser	Asp	Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe	Ser	Gly	Ser
						50		55			60				
Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Gly	Thr	Gln	Ala	Glu
						65		70			75		80		
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Tyr	Asp	Tyr	Ser	Leu	Leu	Val
						85			90			95			
Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys	Ala	Ala
						100			105			110			

Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
 115 120 125
 Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
 130 135 140
 Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu
 145 150 155 160
 Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser
 165 170 175
 Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser
 180 185 190
 Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro
 195 200 205
 Thr Glu Ala
 210

<210> 109
 <211> 211
 <212> PRT
 <213> Homo sapiens

<400> 109
 Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1 5 10 15
 Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
 20 25 30
 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45
 Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60
 Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
 65 70 75 80
 Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Asn Phe His Val
 85 90 95
 Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala
 100 105 110
 Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
 115 120 125
 Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
 130 135 140
 Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu
 145 150 155 160
 Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser
 165 170 175
 Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser
 180 185 190
 Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro
 195 200 205
 Thr Glu Ala
 210

<210> 110
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 110
 Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Met Ile
 85 90 95
 Ala Arg Tyr Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105 110
 Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
 115 120 125
 Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
 130 135 140
 Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
 145 150 155 160
 Lys Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
 165 170 175
 Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
 180 185 190
 His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
 195 200 205
 Lys Thr Val Ala Pro Thr Glu Ala
 210 215

<210> 111
 <211> 213
 <212> PRT
 <213> Homo sapiens

<400> 111
 Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1 5 10 15
 Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
 20 25 30
 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45
 Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60
 Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu

65	70	75	80
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Trp Asp Ile His Pro Phe Asp			
85	90	95	
Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys			
100	105	110	
Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln			
115	120	125	
Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly			
130	135	140	
Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly			
145	150	155	160
Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala			
165	170	175	
Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser			
180	185	190	
Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val			
195	200	205	
Ala Pro Thr Glu Ala			
210			

<210> 112

<211> 213

<212> PRT

<213> Homo sapiens

<400> 112

Asp Ile Val Leu Thr Gln Pro Pro Ser Val Ser Gly Ala Pro Gly Gln			
1	5	10	15
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn			
20	25	30	
Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu			
35	40	45	
Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser			
50	55	60	
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln			
65	70	75	80
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Trp Asp Leu Glu Pro			
85	90	95	
Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys			
100	105	110	
Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln			
115	120	125	
Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly			
130	135	140	
Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly			
145	150	155	160
Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala			
165	170	175	
Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser			
180	185	190	

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
 195 200 205
 Ala Pro Thr Glu Ala
 210

<210> 113

<211> 215

<212> PRT

<213> Homo sapiens

<400> 113

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Val Leu
 85 90 95
 Asp Ser Glu Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110
 Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
 115 120 125
 Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
 130 135 140
 Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
 145 150 155 160
 Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
 165 170 175
 Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
 180 185 190
 Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
 195 200 205
 Thr Val Ala Pro Thr Glu Ala
 210 215

<210> 114

<211> 216

<212> PRT

<213> Homo sapiens

<400> 114

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Pro Ser
 85 90 95
 His Pro Ser Lys Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105 110
 Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
 115 120 125
 Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
 130 135 140
 Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
 145 150 155 160
 Lys Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
 165 170 175
 Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
 180 185 190
 His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
 195 200 205
 Lys Thr Val Ala Pro Thr Glu Ala
 210 215

<210> 115

<211> 214

<212> PRT

<213> Homo sapiens

<400> 115

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Asp Met
 85 90 95
 Gln Phe Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 100 105 110
 Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
 115 120 125
 Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
 130 135 140
 Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala

145	150	155	160
Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala			
165	170	175	
Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg			
180	185	190	
Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr			
195	200	205	
Val Ala Pro Thr Glu Ala			
210			

<210> 116

<211> 215

<212> PRT

<213> Homo sapiens

<400> 116

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln			
1	5	10	15
Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr			
20	25	30	
Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu			
35	40	45	
Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe			
50	55	60	
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu			
65	70	75	80
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Trp Asp Ile Asn			
85	90	95	
His Ala Ile Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln			
100	105	110	
Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu			
115	120	125	
Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr			
130	135	140	
Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys			
145	150	155	160
Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr			
165	170	175	
Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His			
180	185	190	
Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys			
195	200	205	
Thr Val Ala Pro Thr Glu Ala			
210	215		

<210> 117

<211> 215

<212> PRT

<213> Homo sapiens

<400> 117

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Tyr Tyr
 85 90 95
 Asp Tyr Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110
 Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
 115 120 125
 Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
 130 135 140
 Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
 145 150 155 160
 Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
 165 170 175
 Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
 180 185 190
 Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
 195 200 205
 Thr Val Ala Pro Thr Glu Ala
 210 215

<210> 118

<211> 215

<212> PRT

<213> Homo sapiens

<400> 118

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
 50 55 60
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
 65 70 75 80
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ala Asn Asp Phe Pro
 85 90 95
 Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
 100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125
 Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140
 Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160
 Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175
 Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 180 185 190
 Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 195 200 205
 Ser Phe Asn Arg Gly Glu Ala
 210 215

<210> 119
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 119
 Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Trp Asp Asn Leu
 85 90 95
 Lys Met Pro Val Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105 110
 Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
 115 120 125
 Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
 130 135 140
 Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val
 145 150 155 160
 Lys Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys
 165 170 175
 Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser
 180 185 190
 His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu
 195 200 205
 Lys Thr Val-Ala Pro Thr Glu Ala
 210 215

<210> 120
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 120

Asp	Ile	Ala	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln
1					5				10					15	
Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Gly	Tyr
					20				25					30	
Asn	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu
					35				40					45	
Met	Ile	Tyr	Asp	Val	Ser	Asn	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe
					50				55					60	
Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu
					65				70					80	
Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Tyr	Asp	Val	Phe
					85				90					95	
Pro	Ile	Asn	Arg	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly
					100				105					110	
Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	Glu
					115				120					125	
Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	Phe
					130				135					140	
Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro	Val
					145				150					160	
Lys	Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	Lys
					165				170					175	
Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	Ser
					180				185					190	
His	Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val	Glu
					195				200					205	
Lys	Thr	Val	Ala	Pro	Thr	Glu	Ala								
					210				215						

<210> 121
 <211> 213
 <212> PRT
 <213> Homo sapiens

<400> 121

Asp	Ile	Ala	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln
1					5				10					15	
Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Gly	Tyr
					20				25					30	
Asn	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu
					35				40					45	
Met	Ile	Tyr	Asp	Val	Ser	Asn	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe
					50				55					60	
Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu

65	70	75	80
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr	Cys Gln Ser Asp Leu Tyr Phe		
85	90	95	
Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys			
100	105	110	
Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln			
115	120	125	
Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly			
130	135	140	
Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly			
145	150	155	160
Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala			
165	170	175	
Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser			
180	185	190	
Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val			
195	200	205	
Ala Pro Thr Glu Ala			
210			

<210> 122

<211> 214

<212> PRT

<213> Homo sapiens

<400> 122

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln			
1	5	10	15
Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr			
20	25	30	
Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu			
35	40	45	
Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe			
50	55	60	
Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu			
65	70	75	80
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Val Thr			
85	90	95	
Pro Arg Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro			
100	105	110	
Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu			
115	120	125	
Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro			
130	135	140	
Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala			
145	150	155	160
Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala			
165	170	175	
Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg			
180	185	190	

Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
 195 200 205
 Val Ala Pro Thr Glu Ala
 210

<210> 123

<211> 212

<212> PRT

<213> Homo sapiens

<400> 123

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1 5 10 15
 Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
 20 25 30
 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45
 Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60
 Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
 65 70 75 80
 Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Arg Asp Pro Val Gly Phe Pro
 85 90 95
 Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala
 100 105 110
 Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala
 115 120 125
 Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala
 130 135 140
 Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val
 145 150 155 160
 Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser
 165 170 175
 Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 180 185 190
 Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala
 195 200 205
 Pro Thr Glu Ala
 210

<210> 124

<211> 214

<212> PRT

<213> Homo sapiens

<400> 124

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Leu Ser
 85 90 95
 Pro Arg Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 100 105 110
 Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
 115 120 125
 Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
 130 135 140
 Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala
 145 150 155 160
 Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala
 165 170 175
 Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
 180 185 190
 Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
 195 200 205
 Val Ala Pro Thr Glu Ala
 210

<210> 125

<211> 216

<212> PRT

<213> Homo sapiens

<400> 125

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Ser
 85 90 95
 His Tyr Phe Phe Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly
 100 105 110
 Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
 115 120 125
 Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe
 130 135 140
 Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val

145	150	155	160
Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys			
165	170	175	
Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser			
180	185	190	
His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu			
195	200	205	
Lys Thr Val Ala Pro Thr Glu Ala			
210	215		

<210> 126
 <211> 212
 <212> PRT
 <213> Homo sapiens

<400> 126			
Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln			
1	5	10	15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala			
20	25	30	
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr			
35	40	45	
Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser			
50	55	60	
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu			
65	70	75	80
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Leu Arg Tyr Ser His			
85	90	95	
Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala			
100	105	110	
Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala			
115	120	125	
Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala			
130	135	140	
Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val			
145	150	155	160
Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser			
165	170	175	
Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr			
180	185	190	
Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala			
195	200	205	
Pro Thr Glu Ala			
210			

<210> 127
 <211> 214
 <212> PRT
 <213> Homo sapiens

<400> 127

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Leu Arg
 85 90 95
 Asn Arg Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
 100 105 110
 Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
 115 120 125
 Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
 130 135 140
 Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala
 145 150 155 160
 Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala
 165 170 175
 Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
 180 185 190
 Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
 195 200 205
 Val Ala Pro Thr Glu Ala
 210

<210> 128

<211> 215

<212> PRT

<213> Homo sapiens

<400> 128

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Phe Thr
 85 90 95
 Tyr Gly Ser Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
 115 120 125
 Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
 130 135 140
 Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
 145 150 155 160
 Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
 165 170 175
 Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
 180 185 190
 Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
 195 200 205
 Thr Val Ala Pro Thr Glu Ala
 210 215

<210> 129

<211> 215

<212> PRT

<213> Homo sapiens

<400> 129

Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
 20 25 30
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
 50 55 60
 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
 65 70 75 80
 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Phe Asn Asp Ser Pro
 85 90 95
 Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
 100 105 110
 Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125
 Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140
 Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
 145 150 155 160
 Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
 165 170 175
 Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
 180 185 190
 Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
 195 200 205
 Ser Phe Asn Arg Gly Glu Ala
 210 215

<210> 130
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 130
 Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ile Ser
 85 90 95
 Gly Tyr Pro Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110
 Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
 115 120 125
 Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
 130 135 140
 Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
 145 150 155 160
 Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
 165 170 175
 Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
 180 185 190
 Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
 195 200 205
 Thr Val Ala Pro Thr Glu Ala
 210 215

<210> 131
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 131
 Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu

65	70	75	80
Gln Ala Glu Asp	Glu Ala Asp	Tyr Tyr Cys	Gln Ser Arg Asp
85	90	95	Leu Tyr
Tyr Val Tyr Tyr Val Phe Gly Gly	Gly Thr Lys Leu Thr Val	Leu Gly	
100	105	110	
Gln Pro Lys Ala Ala Pro Ser Val	Thr Leu Phe Pro Pro Ser Ser	Glu	
115	120	125	
Glu Leu Gln Ala Asn Lys Ala	Thr Leu Val Cys Leu Ile Ser Asp Phe		
130	135	140	
Tyr Pro Gly Ala Val Thr Val Ala Trp	Lys Ala Asp Ser Ser Pro Val		
145	150	155	160
Lys Ala Gly Val Glu Thr Thr Pro Ser	Lys Gln Ser Asn Asn Lys		
165	170	175	
Tyr Ala Ala Ser Ser Tyr Leu Ser	Leu Thr Pro Glu Gln Trp Lys Ser		
180	185	190	
His Arg Ser Tyr Ser Cys Gln Val	Thr His Glu Gly Ser Thr Val Glu		
195	200	205	
Lys Thr Val Ala Pro Thr Glu Ala			
210	215		

<210> 132

<211> 211

<212> PRT

<213> Homo sapiens

<400> 132

Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln			
1	5	10	15
Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala			
20	25	30	
Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr			
35	40	45	
Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser			
50	55	60	
Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu			
65	70	75	80
Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Arg Ser Met Trp Val			
85	90	95	
Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala			
100	105	110	
Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn			
115	120	125	
Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val			
130	135	140	
Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu			
145	150	155	160
Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser			
165	170	175	
Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr Ser			
180	185	190	

Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro
 195 200 205
 Thr Glu Ala
 210

<210> 133
 <211> 215
 <212> PRT
 <213> Homo sapiens

<400> 133
 Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Trp Asp Val Gln
 85 90 95
 Thr Asp Lys Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110
 Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
 115 120 125
 Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
 130 135 140
 Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
 145 150 155 160
 Ala Gly Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
 165 170 175
 Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
 180 185 190
 Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
 195 200 205
 Thr Val Ala Pro Thr Glu Ala
 210 215

<210> 134
 <211> 212
 <212> PRT
 <213> Homo sapiens

<400> 134
 Asp Ile Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln
 1 5 10 15
 Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
 20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45
 Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60
 Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
 65 70 75 80
 Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Trp Asp Pro Ser His Tyr Tyr
 85 90 95
 Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala
 100 105 110
 Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala
 115 120 125
 Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala
 130 135 140
 Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val
 145 150 155 160
 Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser
 165 170 175
 Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 180 185 190
 Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala
 195 200 205
 Pro Thr Glu Ala
 210

<210> 135

<211> 215

<212> PRT

<213> Homo sapiens

<400> 135

Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ile Met
 85 90 95
 Pro Glu Arg Val Phe Gly Gly Thr Lys Leu Thr Val Leu Gly Gln
 100 105 110
 Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
 115 120 125
 Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr
 130 135 140
 Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys

145	150	155	160												
Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	Lys	Tyr
				165					170					175	
Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	Ser	His
					180			185				190			
Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val	Glu	Lys
					195			200				205			
Thr	Val	Ala	Pro	Thr	Glu	Ala									
		210			215										

<210> 136

<211> 215

<212> PRT

<213> Homo sapiens

<400> 136

Asp	Ile	Ala	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln
1					5				10				15		
Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Gly	Tyr
						20			25				30		
Asn	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu
						35			40				45		
Met	Ile	Tyr	Asp	Val	Ser	Asn	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe
						50			55				60		
Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu
						65			70				75		80
Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Met	Asp	Phe	Arg
						85			90				95		
Leu	Met	His	Val	Phe	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	
						100			105				110		
Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	Glu	Glu
						115			120				125		
Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	Phe	Tyr
						130			135				140		
Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro	Val	Lys
						145			150				155		160
Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	Lys	Tyr
						165			170				175		
Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	Ser	His
						180			185				190		
Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val	Glu	Lys
						195			200				205		
Thr	Val	Ala	Pro	Thr	Glu	Ala									
		210			215										

<210> 137

<211> 215

<212> PRT

<213> Homo sapiens

<400> 137

Asp	Ile	Ala	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln
1			5				10						15		
Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Gly	Tyr
	20						25						30		
Asn	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu
	35						40						45		
Met	Ile	Tyr	Asp	Val	Ser	Asn	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe
	50						55						60		
Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu
	65						70						75		80
Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Phe	Asp	Met	Ile
							85						90		95
His	Pro	Tyr	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln
							100						105		110
Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	Glu	Glu
							115						120		125
Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	Phe	Tyr
	130						135						140		
Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro	Val	Lys
	145						150						155		160
Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	Lys	Tyr
							165						170		175
Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	Ser	His
							180						185		190
Arg	Ser	Tyr	Ser	Cys	Gln	Val	Thr	His	Glu	Gly	Ser	Thr	Val	Glu	Lys
							195						200		205
Thr	Val	Ala	Pro	Thr	Glu	Ala									
	210						215								

<400> 138

<211> 213

<212> PRT

<213> Homo sapiens

<400> 138

Asp	Ile	Ala	Leu	Thr	Gln	Pro	Ala	Ser	Val	Ser	Gly	Ser	Pro	Gly	Gln
1			5				10						15		
Ser	Ile	Thr	Ile	Ser	Cys	Thr	Gly	Thr	Ser	Ser	Asp	Val	Gly	Gly	Tyr
	20						25						30		
Asn	Tyr	Val	Ser	Trp	Tyr	Gln	Gln	His	Pro	Gly	Lys	Ala	Pro	Lys	Leu
	35						40						45		
Met	Ile	Tyr	Asp	Val	Ser	Asn	Arg	Pro	Ser	Gly	Val	Ser	Asn	Arg	Phe
	50						55						60		
Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Ser	Gly	Leu
	65						70						75		80
Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Ser	Asp	Phe	Pro	Val
							85						90		95
Met	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	Gln	Pro	Lys
							100						105		110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
 115 120 125
 Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
 130 135 140
 Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
 145 150 155 160
 Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
 165 170 175
 Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
 180 185 190
 Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
 195 200 205
 Ala Pro Thr Glu Ala
 210

<210> 139
 <211> 213
 <212> PRT
 <213> Homo sapiens

<400> 139
 Asp Ile Ala Leu Thr Gln Pro Ala Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15
 Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
 20 25 30
 Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45
 Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
 50 55 60
 Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
 65 70 75 80
 Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Asp Asn Pro Tyr
 85 90 95
 Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys
 100 105 110
 Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
 115 120 125
 Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
 130 135 140
 Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
 145 150 155 160
 Val Glu Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
 165 170 175
 Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
 180 185 190
 Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
 195 200 205
 Ala Pro Thr Glu Ala
 210

100	105	110
Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr		
115	120	125
Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser		
130	135	140
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu		
145	150	155
Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His		160
165	170	175
Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser		
180	185	190
Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys		
195	200	205
Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu		
210	215	220
Pro Lys Ser Glu Phe		
225		

<210> 156

<211> 220

<212> PRT

<213> Homo sapiens

<400> 156

Gln Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly		
1	5	10
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr		
20	25	30
Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val		
35	40	45
Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val		
50	55	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr		
65	70	75
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys		
85	90	95
Ala Arg Leu Ile Gly Tyr Phe Asp Leu Trp Gly Gln Gly Thr Leu Val		
100	105	110
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala		
115	120	125
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu		
130	135	140
Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly		
145	150	155
Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser		
165	170	175
Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu		
180	185	190
Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr		
195	200	205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu Phe
 210 215 220

<210> 157

<211> 225

<212> PRT

<213> Homo sapiens

<400> 157

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30
 Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Leu Thr Asn Tyr Phe Asp Ser Ile Tyr Tyr Asp His Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu
 210 215 220

Phe

225

<210> 158

<211> 225

<212> PRT

<213> Homo sapiens

<400> 158

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Leu Val Gly Gly Tyr Asp Leu Met Phe Asp Ser Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu
 210 215 220
 Phe
 225

<210> 159
 <211> 226
 <212> PRT
 <213> Homo sapiens

<400> 159
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30
 Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Tyr Val Thr Tyr Gly Tyr Asp Asp Tyr His Phe Asp Tyr Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr

130	135	140
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr		
145	150	155
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro		160
165	170	175
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr		
180	185	190
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn		
195	200	205
His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser		
210	215	220
Glu Phe		
225		

<210> 160

<211> 219

<212> PRT

<213> Homo sapiens

<400> 160

1	5	10	15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr			
20	25	30	
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met			
35	40	45	
Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe			
50	55	60	
Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr			
65	70	75	80
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys			
85	90	95	
Ala Arg Ser Gly Tyr Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr			
100	105	110	
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro			
115	120	125	
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val			
130	135	140	
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala			
145	150	155	160
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly			
165	170	175	
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly			
180	185	190	
Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys			
195	200	205	
Val Asp Lys Lys Val Glu Pro Lys Ser Glu Phe			
210	215		

<210> 161

<211> 231
 <212> PRT
 <213> Homo sapiens

<400> 161

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1					5				10				15		
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr
					20				25				30		
Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
					35				40				45		
Gly	Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe
					50				55				60		
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	Thr	Ala	Tyr
					65				70				75		80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
					85				90				95		
Ala	Arg	Tyr	Ile	Gly	Tyr	Thr	Asn	Val	Met	Asp	Ile	Arg	Pro	Gly	Phe
					100				105				110		
Tyr	Leu	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala
					115				120				125		
Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser
					130				135				140		
Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe
					145				150				155		160
Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly
					165				170				175		
Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu
					180				185				190		
Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr
					195				200				205		
Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys
					210				215				220		
Val	Glu	Pro	Lys	Ser	Glu	Phe									
					225				230						

<210> 162
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 162

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
1					5				10				15		
Ser	Leu	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Ser	Phe	Thr	Ser	Tyr
					20				25				30		
Trp	Ile	Gly	Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Met
					35				40				45		
Gly	Ile	Ile	Tyr	Pro	Gly	Asp	Ser	Asp	Thr	Arg	Tyr	Ser	Pro	Ser	Phe
					50				55				60		

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Phe Arg Ala Tyr Gly Asp Asp Phe Tyr Phe Asp Val Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190
 Pro Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu
 210 215 220
 Phe
 225

<210> 163
 <211> 228
 <212> PRT
 <213> Homo sapiens

<400> 163
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30
 Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Ile Met Trp Ser Asp Tyr Gly Gln Leu Val Lys Gly Gly Asp
 100 105 110
 Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
 115 120 125
 Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
 130 135 140
 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 145 150 155 160
 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr

	165		170		175										
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val
				180				185				190			
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn
				195			200			205					
Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro
				210			215			220					
Lys	Ser	Glu	Phe												
				225											

<210> 164

<211> 224

<212> PRT

<213> Homo sapiens

<400> 164

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
1					5				10				15		
Ser	Leu	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Ser	Phe	Thr	Ser	Tyr
					20				25			30			
Trp	Ile	Gly	Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Met
					35				40			45			
Gly	Ile	Ile	Tyr	Pro	Gly	Asp	Ser	Asp	Thr	Arg	Tyr	Ser	Pro	Ser	Phe
					50				55			60			
Gln	Gly	Gln	Val	Thr	Ile	Ser	Ala	Asp	Lys	Ser	Ile	Ser	Thr	Ala	Tyr
					65				70			75			80
Leu	Gln	Trp	Ser	Ser	Leu	Lys	Ala	Ser	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
					85				90			95			
Ala	Arg	Tyr	Tyr	Val	Thr	Asp	Thr	Ala	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln
					100				105			110			
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
					115				120			125			
Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala
					130				135			140			
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
					145				150			155			160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
					165				170			175			
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
					180				185			190			
Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys
					195				200			205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Glu	Phe
					210				215			220			

<210> 165

<211> 224

<212> PRT

<213> Homo sapiens

<400> 165

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30
 Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg His Asp Phe Asp Gly Ser Ile Phe Met Asp Phe Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu Phe
 210 215 220

<210> 166

<211> 225

<212> PRT

<213> Homo sapiens

<400> 166

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30
 Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Tyr Ala Gly His Gln Tyr Glu Phe Phe Asp Phe Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190
 Pro Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu
 210 215 220
 Phe
 225

<210> 167

<211> 224

<212> PRT

<213> Homo sapiens

<400> 167

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30
 Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Leu Tyr Ala Asp Ala Asp Ile Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu Phe

210

215

220

<210> 168
 <211> 222
 <212> PRT
 <213> Homo sapiens

<400> 168
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30
 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Thr Lys Tyr Val Gly Ser Glu Asp Val Trp Gly Gln Gly Thr
 100 105 110
 Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 115 120 125
 Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 130 135 140
 Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 145 150 155 160
 Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 165 170 175
 Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 180 185 190
 Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 195 200 205
 Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu Phe
 210 215 220

<210> 169
 <211> 222
 <212> PRT
 <213> Homo sapiens

<400> 169
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30
 Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe

50	55	60													
Gln	Gly	Gln	Val	Thr	Ile	Ser	Ala	Asp	Lys	Ser	Ile	Ser	Thr	Ala	Tyr
65					70					75				80	
Leu	Gln	Trp	Ser	Ser	Leu	Lys	Ala	Ser	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
					85					90			95		
Ala	Arg	Tyr	Arg	Tyr	Pro	His	Met	Phe	Asp	Phe	Trp	Gly	Gln	Gly	Thr
					100					105			110		
Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro
					115					120			125		
Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly
					130					135			140		
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn
145					150					155			160		
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
					165					170			175		
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
					180					185			190		
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser
					195					200			205		
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Glu	Phe		
					210					215			220		

<210> 170

<211> 224

<212> PRT

<213> Homo sapiens

<400> 170

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
1					5					10			15		
Ser	Leu	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Ser	Phe	Thr	Ser	Tyr
					20					25			30		
Trp	Ile	Gly	Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Met
					35					40			45		
Gly	Ile	Ile	Tyr	Pro	Gly	Asp	Ser	Asp	Thr	Arg	Tyr	Ser	Pro	Ser	Phe
					50					55			60		
Gln	Gly	Gln	Val	Thr	Ile	Ser	Ala	Asp	Lys	Ser	Ile	Ser	Thr	Ala	Tyr
65					70					75			80		
Leu	Gln	Trp	Ser	Ser	Leu	Lys	Ala	Ser	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
					85					90			95		
Ala	Arg	Leu	Phe	Ala	Gly	Leu	Glu	Leu	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln
					100					105			110		
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
					115					120			125		
Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala
					130					135			140		
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150					155			160		
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
					165					170			175		

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu Phe
 210 215 220

<210> 171

<211> 221

<212> PRT

<213> Homo sapiens

<400> 171

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Ala Ile Ser Gly Ser Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Gly Gly Phe Phe Asn Met Asp Tyr Trp Gly Gln Gly Thr Leu
 100 105 110
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125
 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190
 Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205
 Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu Phe
 210 215 220

<210> 172

<211> 223

<212> PRT

<213> Homo sapiens

<400> 172

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30
 Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Gly Tyr Ile Pro Tyr His Leu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125
 Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140
 Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160
 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175
 Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190
 Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 195 200 205
 Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu Phe
 210 215 220

<210> 173

<211> 225

<212> PRT

<213> Homo sapiens

<400> 173

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30
 Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Tyr Tyr Gly Phe Glu Tyr Asp Leu Leu Phe Asp Asn Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala

130	135	140													
Ala	Leu	Gly	Cys	'Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
145				150					155					160	
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
				165				170					175		
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
				180				185				190			
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
				195			200				205				
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Gl
	210				215					220					
Phe															
225															

<210> 174

<211> 221

<212> PRT

<213> Homo sapiens

<400> 174

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser	
1					5				10				15			
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr	
					20				25				30			
Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
					35				40				45			
Gly	Trp	Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr	Ala	Gln	Lys	Phe	
					50				55				60			
Gln	Gly	Arg	Val	Thr	Met	Thr	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr	
					65				70				75		80	
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
					85				90				95			
Ala	Arg	Ile	Thr	Tyr	Ile	Gly	Tyr	Asp	Phe	Trp	Gly	Gln	Gly	Thr	Leu	
					100				105				110			
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	
					115				120				125			
Ala	Pro	Ser	Ser	Lys	Ser	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys
					130				135				140			
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	
					145				150				155		160	
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	
					165				170				175			
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	
					180				185				190			
Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	
					195				200				205			
Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Glu	Phe				
					210				215				220			

<210> 175

<211> 220
 <212> PRT
 <213> Homo sapiens

<400> 175

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1					5				10				15		
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr
					20				25				30		
Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
					35				40			45			
Gly	Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe
					50				55			60			
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Glu	Ser	Thr	Ser	Thr	Ala	Tyr
					65				70			75			80
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
					85				90			95			
Ala	Arg	Gln	Glu	Trp	Tyr	Met	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val
					100				105			110			
Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala
					115				120			125			
Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu
					130				135			140			
Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly
					145				150			155			160
Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser
					165				170			175			
Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu
					180				185			190			
Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr
					195				200			205			
Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Glu	Phe				
					210				215			220			

<210> 176
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 176

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
1					5				10				15		
Ser	Leu	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Ser	Phe	Thr	Ser	Tyr
					20				25			30			
Trp	Ile	Gly	Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Met
					35				40			45			
Gly	Ile	Ile	Tyr	Pro	Gly	Asp	Ser	Asp	Thr	Arg	Tyr	Ser	Pro	Ser	Phe
					50				55			60			
Gln	Gly	Gln	Val	Thr	Ile	Ser	Ala	Asp	Lys	Ser	Ile	Ser	Thr	Ala	Tyr
					65				70			75			80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Leu Tyr Pro Glu Asp Leu Ile Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu Phe
 210 215 220

<210> 177

<211> 231

<212> PRT

<213> Homo sapiens

<400> 177

Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15
 Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
 20 25 30
 Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
 35 40 45
 Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
 50 55 60
 Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
 65 70 75 80
 Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
 85 90 95
 Tyr Tyr Cys Ala Arg Trp Met Thr Pro Pro Gly His Tyr Tyr Gly Tyr
 100 105 110
 Thr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
 115 120 125
 Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
 130 135 140
 Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
 145 150 155 160
 Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
 165 170 175
 Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
 180 185 190
 Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr

195	200	205
Ile Cys Asn Val Asn His Lys	Pro Ser Asn Thr Lys	Val Asp Lys Lys
210	215	220
Val Glu Pro Lys Ser Glu Phe		
225	230	

<210> 178
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 178
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30
 Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Leu Arg Val His Asp Tyr Ala Met Tyr Phe Asp Leu Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125
 Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140
 Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190
 Pro Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu
 210 215 220
 Phe
 225

<210> 179
 <211> 226
 <212> PRT
 <213> Homo sapiens

<400> 179
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu

1	5	10	15												
Ser	Leu	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Ser	Phe	Thr	Ser	Tyr
20	25	30													
Trp	Ile	Gly	Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Met
35	40	45													
Gly	Ile	Ile	Tyr	Pro	Gly	Asp	Ser	Asp	Thr	Arg	Tyr	Ser	Pro	Ser	Phe
50	55	60													
Gln	Gly	Gln	Val	Thr	Ile	Ser	Ala	Asp	Lys	Ser	Ile	Ser	Thr	Ala	Tyr
65	70	75	80												
Leu	Gln	Trp	Ser	Ser	Leu	Lys	Ala	Ser	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
85	90	95													
Ala	Arg	Phe	Val	Ser	Tyr	Asn	Gly	Ser	Val	Pro	Tyr	Phe	Asp	Tyr	Trp
100	105	110													
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro
115	120	125													
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
130	135	140													
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
145	150	155	160												
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
165	170	175													
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
180	185	190													
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
195	200	205													
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser
210	215	220													
Glu	Phe														
225															

<210> 180

<211> 224

<212> PRT

<213> Homo sapiens

<400> 180

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Glu
1	5	10	15												
Ser	Leu	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Ser	Phe	Thr	Ser	Tyr
20	25	30													
Trp	Ile	Gly	Trp	Val	Arg	Gln	Met	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Met
35	40	45													
Gly	Ile	Ile	Tyr	Pro	Gly	Asp	Ser	Asp	Thr	Arg	Tyr	Ser	Pro	Ser	Phe
50	55	60													
Gln	Gly	Gln	Val	Thr	Ile	Ser	Ala	Asp	Lys	Ser	Ile	Ser	Thr	Ala	Tyr
65	70	75	80												
Leu	Gln	Trp	Ser	Ser	Leu	Lys	Ala	Ser	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
85	90	95													
Ala	Arg	Ile	Ile	Gly	Asp	Tyr	Val	Ile	Phe	Phe	Asp	Val	Trp	Gly	Gln
100	105	110													

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu Phe
 210 215 220

<210> 181

<211> 224

<212> PRT

<213> Homo sapiens

<400> 181

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30
 Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Leu Phe Thr Tyr Pro Phe Leu Tyr Phe Asp Val Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu Phe
 210 215 220

<210> 182
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 182
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
 1 5 10 15
 Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30
 Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45
 Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
 50 55 60
 Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Ala Arg Ile Leu Thr Gly His Val Leu Leu Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu Phe
 210 215 220

<210> 183
 <211> 27
 <212> DNA
 <213> Homo sapiens

<400> 183
 cagagctatg actatcagca gtttact

27

<210> 184
 <211> 26
 <212> DNA
 <213> Homo sapiens

<400> 184
 cagagctatg actttaagac ttatct

26

<210> 185
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<212> DNA
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<400> 185
cagagctatg actttcttcg ttttgc 26

<210> 186
<211> 27
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<400> 186
cagagctatg acttttattaa tgttatt 27

<210> 187
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<400> 187
cagagctatg actttgttcg ttttgc 27

<210> 188
<211> 27
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<400> 188
cagagctatg acttttataa gtttaat 27

<210> 189
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<400> 189
cagagctatg actttcgatcg tttttct 27

<210> 190
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<400> 190
cagagccgtg actttaatcg tggcct 27

<210> 191

<211> 24
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<400> 191
cagagctatg accagcgtaa gtgg 24

<210> 192
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<400> 192
cagcagcttt atggtaacttc tgtt 24

<210> 193
<211> 27
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<400> 193
cagagctatg acggttttaa gactcat 27

<210> 194
<211> 24
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<400> 194
cagagctatg actattctct tctt 24

<210> 195
<211> 24
<212> DNA
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<400> 195
cagagctatg actttaattt tcatt 24

<210> 196
<211> 30
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<400> 196
cagagctatg acatgattgc tcgttacct 30

<210> 197
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<400> 197
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<210> 198
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<400> 198
cagagctggg accttgagcc ttat 24

<210> 199
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<400> 199
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<210> 200
<211> 30
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<400> 200
cagagctatg acccttctca tccttctaag 30

<210> 201
<211> 24
<212> DNA
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<400> 201
cagagctatg acgatatgca gttt 24

<210> 202
<211> 27
<212> DNA
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<400> 202
cagagctggg acatthaatca tgctatt 27

<210> 203
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<400> 203	
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<210> 204	
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<400> 204	
cagcaggcta atgatttcc tatt	24
<210> 205	
<211> 30	
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cagagctggg acaatcttaa gatgcctgtt	30
<210> 206	
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<212> DNA	
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<400> 206	
cagagctatg acgttttcc tattaatcgt	30
<210> 207	
<211> 21	
<212> DNA	
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<400> 207	
cagagcgatc tttatttcc t	21
<210> 208	
<211> 24	
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cagagctatg acgttactcc tcgt	24
<210> 209	
<211> 27	
<212> DNA	
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<400> 209	
cagagccgtg accctgttgg ttttct	27

<210> 210
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<400> 210
cagagctatg acctttctcc tcgt 24

<210> 211
<211> 30
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<400> 211
cagagctatg acttttctca ttatttttt 30

<210> 212
<211> 27
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<400> 212
cagagctatg accttcgtta ttctcat 27

<210> 213
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<400> 213
cagagctatg accttcgtaa tcgt 24

<210> 214
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<400> 214
cagagctatg actttactta tggttct 27

<210> 215
<211> 24
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<400> 215
cagcagttta atgattctcc ttat 24

<210> 216

<211> 27
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<400> 216
cagagctatg acatttctgg ttatcct 27

<210> 217
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<400> 217
cagagccgtg acctttattta tgtttattat 30

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cagagctatg accgttctat gtgg 24

<210> 219
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<400> 219
cagagctggg acgttcagac tgataag 27

<210> 220
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<400> 220
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<210> 221
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<400> 221
cagagctatg acattatgcc tgagcgt 27

<210> 222
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<213> Homo sapiens

<400> 222

cagagcatgg actttcgctc tatgcat

27

<210> 223

<211> 27

<212> DNA

<213> Homo sapiens

<400> 223

cagagcttg acatgattca tccttat

27

<210> 224

<211> 21

<212> DNA

<213> Homo sapiens

<400> 224

cagagcgact ttccctgttat g

21

<210> 225

<211> 21

<212> DNA

<213> Homo sapiens

<400> 225

cagagcgaca atccttatct t

21

<210> 226

<211> 12

<212> DNA

<213> Homo sapiens

<400> 226

tttatggata tt

12

<210> 227

<211> 12

<212> DNA

<213> Homo sapiens

<400> 227

ggttttgatt at

12

<210> 228

<211> 12

<212> DNA

<213> Homo sapiens

<400> 228
tttcttgata tt 12

<210> 229
<211> 24
<212> DNA
<213> Homo sapiens

<400> 229
acttttccta ttgatgtga ttct 24

<210> 230
<211> 15
<212> DNA
<213> Homo sapiens

<400> 230
ggtcatgttg attat 15

<210> 231
<211> 27
<212> DNA
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<400> 231
tattggcgtg gtctttcttt tgatatt 27

<210> 232
<211> 12
<212> DNA
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<400> 232
tttttgatt at 12

<210> 233
<211> 36
<212> DNA
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<400> 233
ggtccttatt gggctgttta tccttatttt gatttt 36

<210> 234
<211> 33
<212> DNA
<213> Homo sapiens

<400> 234
cttgatactt attatccctga tcttttgat tat 33

<210> 235
<211> 21
<212> DNA
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<400> 235
acttattatt attttggattc t 21

<210> 236
<211> 33
<212> DNA
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<400> 236
tatatggctt atatggctga ggctattgat gtt 33

<210> 237
<211> 51
<212> DNA
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<400> 237
cttggggta ttgttggta taagcctgat gagcttcttt attttggatgt t 51

<210> 238
<211> 27
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<400> 238
tatggtgctt attttggtct tgattat 27

<210> 239
<211> 27
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<400> 239
ggtagatgtg atatttcttt tgattat 27

<210> 240
<211> 21
<212> DNA
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<400> 240
tattatcttc ttcttgattt t 21

<210> 241

<211> 48
<212> DNA
<213> Homo sapiens

<400> 241
tggtctgatc agtcttatca ttattattgg catccttatt ttgatgtt 48

<210> 242
<211> 21
<212> DNA
<213> Homo sapiens

<400> 242
cttattgggtt attttgatct t 21

<210> 243
<211> 36
<212> DNA
<213> Homo sapiens

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<400> 273

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<210> 274

<211> 660

<212> DNA

<213> Homo sapiens

<400> 274

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tatagcctga	gcagcgttgt	gaccgtgccc	agcagcagct	tagcactca	gacctatatt	600
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<210> 275

<211> 645

<212> DNA

<213> Homo sapiens

<400> 275

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gttgtgaccg	tgccgagcag	cagcttaggc	actcagacct	atatttgcaa	cgtgaaccat	600
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<210> 276

<211> 669
 <212> DNA
 <213> Homo sapiens

<400> 276

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agcggcctgt	atagcctgag	cagcgtgtg	accgtccga	gcagcagctt	aggcactctag	600
acctatattt	gcaacgtgaa	ccataaaccg	agcaacacca	aagtggataa	aaaagtggaa	660
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<210> 277
 <211> 666
 <212> DNA
 <213> Homo sapiens

<400> 277

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ggcctgtata	gcctgagcag	cgttgtgacc	gtgccgagca	gcagcttagg	cactcagacc	600
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<210> 278
 <211> 654
 <212> DNA
 <213> Homo sapiens

<400> 278

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ggtccaagcg	tgtttccgct	ggctccgagc	agcaaaagca	ccagcggcgg	cacggctgcc	420

ctgggctgcc	tggtaaaga	ttatccc	gaaccagtca	ccgtgagctg	gaacagcggg	480
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ctgagcagcg	ttgtgaccgt	gccgagcagc	agcttaggca	ctcagaccta	tatttgca	600
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<210> 279

<211> 666

<212> DNA

<213> Homo sapiens

<400> 279

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<210> 280

<211> 684

<212> DNA

<213> Homo sapiens

<400> 280

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<210> 281

<211> 660

<212> DNA

<213> Homo sapiens

<400> 281

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<210> 282

<211> 669

<212> DNA

<213> Homo sapiens

<400> 282

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<210> 283

<211> 654

<212> DNA

<213> Homo sapiens

<400> 283

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<211> 681

<212> DNA

<213> Homo sapiens

<400> 284

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<211> 654

<212> DNA

<213> Homo sapiens

<400> 285

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gc当地	gc当地	taccttccg	gc当地	aaagc当地	c当地	540
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<210> 286

<211> 669

<212> DNA

<213> Homo sapiens

<400> 286

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ggc当地	ctgccc当地	ctgccc当地	aaagattt	tccc当地	agtc当地	480
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<211> 687

<212> DNA

<213> Homo sapiens

<400> 290

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<210> 291

<211> 669

<212> DNA

<213> Homo sapiens

<400> 291

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<210> 292

<211> 678

<212> DNA

<213> Homo sapiens

<400> 292

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<210> 293

<211> 666

<212> DNA

<213> Homo sapiens

<400> 293

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<210> 294

<211> 666

<212> DNA

<213> Homo sapiens

<400> 294

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<210> 298

<211> 660

<212> DNA

<213> Homo sapiens

<400> 298

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<210> 299

<211> 666

<212> DNA

<213> Homo sapiens

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<211> 657

<212> DNA

<213> Homo sapiens

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<211> 663

<212> DNA

<213> Homo sapiens

<400> 301

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attccttatac	atcttttga	ttattgggc	caaggcaccc	tggtagcgg	tagctcagcg	360
tc当地	gtccaagcgt	gttccgctg	gctccgagca	gcaaaagcac	cagcggcggc	420
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<210> 302

<211> 669

<212> DNA

<213> Homo sapiens

<400> 302

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<211> 687

<212> DNA

<213> Homo sapiens

<400> 306

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<211> 669

<212> DNA

<213> Homo sapiens

<400> 307

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<211> 672

<212> DNA

<213> Homo sapiens

<400> 308

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<210> 309

<211> 666

<212> DNA

<213> Homo sapiens

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<210> 310

<211> 609

<212> DNA

<213> Homo sapiens

<400> 310

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<212> DNA

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<211> 638

<212> DNA

<213> Homo sapiens

<400> 315

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<211> 645

<212> DNA

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<212> DNA

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<400> 317

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<210> 318

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<213> Homo sapiens

<400> 318

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ctgtttccgc cgagcagcga agaattgcag gccaacaag cgaccctggt gtgcctgatt	420
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gcgggagtgg agaccaccac accctccaaa caaagcaaca acaagtacgc gcccagcagc	540
tatctgagcc tgacgcctga gcagtggaaag tcccacagaa gctacagctg ccaggtcacg	600
catgagggga gcaccgtgga aaaaaccgtt gcgccgac	638

<210> 319

<211> 642

<212> DNA

<213> Homo sapiens

<400> 319

gatatcg	tgacccagcc	gccttcagt	agtggcgac	caggtcag	tgtgaccatc	60
tcgtgt	cgagcag	caacattgg	agcaactat	tgactgtt	ccagcagtt	120
ccgggac	cgccgaa	act gctgatt	gataaca	agcgtcc	aggcg	180
gatcg	cgatccaa	aaggcc	agcgcgag	ttgcgatt	ggcctgcaa	240
agcaag	aaggatt	ttattg	ccgtgact	ttaatcg	tcctgtgtt	300
ggccg	cgaagtt	cg	cagccgaa	ccgcacc	tg	360
tttcc	gcagcga	attgcagg	aacaaagc	ccctgg	cctgatt	420
gactt	cgggag	cg	gacagtgg	tggaaagg	atagcag	480
ggagtgg	ccaccac	ctccaa	agcaaca	agtac	cgcc	540
ctgag	cctgag	gtgg	aaagtcc	cacaga	actg	600
gaggg	gagca	ccgtgg	aaaa	aaccgtt	ccgact	642

<210> 320

<211> 639

<212> DNA

<213> Homo sapiens

<400> 320

gatatcg	tgacccagcc	gccttcagt	agtggcgac	caggtcag	tgtgaccatc	60
tcgtgt	cgagcag	caacattgg	agcaactat	tgactgtt	ccagcagtt	120
ccgggac	cgccgaa	act gctgatt	gataaca	agcgtcc	aggcg	180
gatcg	cgatccaa	aaggcc	agcgcgag	ttgcgatt	ggcctgcaa	240
agcaag	aaggatt	ttattg	ccgtgact	agctatg	gtgtttgg	300
ggccg	cacga	atttacc	tcttgg	ccgaaag	caccgagt	360
ccggc	gagca	attt	gcaggc	aaagcgac	tggtg	420
ttt	atccg	gagcc	gt	gagata	gcagcc	480
gtgg	gagac	ccacacc	caa	acaaca	acgccc	540
agcc	tgc	tgc	aa	gactaca	cagctat	600
ggg	gac	ccg	tt	ggatc	ca	639

<210> 321

<211> 672

<212> DNA

<213> Homo sapiens

<400> 321

gatatcg	tgacccagag	ccggcgacc	ctgagcctgt	ctccggcga	acgtgcgacc	60
ctgag	ctgca	gagc	gagcgtg	agcag	cttcc	120
ccagg	tcaag	cacc	cgct	attat	tttgg	180
gcgcg	tttta	gccc	ctct	atcc	gggt	240
cctg	aaact	tttgc	actt	tttac	cc	300
cagg	tgac	tttgc	tttgc	tttgc	tttgc	360
ccg	gat	tttgc	tttgc	tttgc	tttgc	420
tat	ccgc	tttgc	tttgc	tttgc	tttgc	480
cagg	aaag	tttgc	tttgc	tttgc	tttgc	540
acc	tgc	tttgc	tttgc	tttgc	tttgc	600
ggt	tgc	tttgc	tttgc	tttgc	tttgc	660

ggagaaaata aa	672
<210> 322	
<211> 642	
<212> DNA	
<213> Homo sapiens	
<400> 322	
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ccccggacgg cgccgaaact gctgatattt gataacaacc agcgccctc aggctgccc	180
gatcgttta gcggatccaa aagcggcacc agcgcgagcc ttgcgattac gggctgcaa	240
agcgaagacg aagcggattt ttattggcag agctatgacg gtttaagac tcatgtgttt	300
ggccggcggca cgaagttaac cgttcttggc cagccgaaag ccgcaccgag tgtgacgctg	360
tttccggcga gcagcgaaga attgcaggcg aacaaagcga ccctgggtgt cctgattagc	420
gactttatc cgggagccgt gacagtggcc tggaggcag atagcagccc cgtcaaggcg	480
ggagtggaga ccaccacacc ctccaaacaa agcaacaaca agtacgcggc cagcagctat	540
ctgagcctga cgcctgagca gtggaaagtcc cacagaagct acagtcgcca ggtcacgcat	600
gaggggagca ccgtggaaaa aaccgttgcg ccgactgagg cc	642
<210> 323	
<211> 633	
<212> DNA	
<213> Homo sapiens	
<400> 323	
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tcgtgttagcg gcgtatgcgt gggcgataaa tacgcgagct ggtaccagca gaaacccggg	120
caggcgccag ttctgggtat ttatgtatgt tctgaccgtc cctcaggcat cccggaaacgc	180
tttagcggat ccaacagcgg caacaccgcg accctgacca tttagcggcac tcaggcggaa	240
gacgaagcgg attattattt ccagagctat gactatttc ttctgggttt tggcggcggc	300
acgaagttaa ccgttcttgg ccagccgaaa gccgcaccga gtgtgacgct gttccgcgg	360
agcagcgaag aattgcaggc gaacaaagcg accctgggtt gcctgatttag cgactttat	420
ccgggagccg tgacagtggc ctggaaaggca gatagcagcc ccgtcaaggc gggagtgag	480
accaccacac cctccaaaca aagcaacaac aagtacgcgg ccagcagcta tctgacgcctg	540
acgcctgagc agtggaaagtc ccacagaagc tacagtcgac aggtcacgca tgaggggagc	600
accgtggaaa aaaccgttgc gccgactgag gcc	633
<210> 324	
<211> 633	
<212> DNA	
<213> Homo sapiens	
<400> 324	
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tcgtgttagcg gcgtatgcgt gggcgataaa tacgcgagct ggtaccagca gaaacccggg	120
caggcgccag ttctgggtat ttatgtatgt tctgaccgtc cctcaggcat cccggaaacgc	180
tttagcggat ccaacagcgg caacaccgcg accctgacca tttagcggcac tcaggcggaa	240
gacgaagcgg attattattt ccagagctat gactttaaatt ttcatgtgtt tggcggcggc	300
acgaagttaa ccgttcttgg ccagccgaaa gccgcaccga gtgtgacgct gttccgcgg	360

agcagcgaag aattgcaggc gaacaaagcg accctggtgt gcctgattag cgacttttat	420
ccgggagccg tgacagtggc ctgaaaggca gatagcagcc ccgtaaggc gggagtggag	480
accaccacac cctccaaaca aagaacaac aagtacgccc ccagcagcta tctgagccctg	540
acgcctgagc agtggaaatc ccacagaagc tacagctgcc aggtcagcga tgaggggagc	600
accgtggaaa aaaccgttgc gcccactgag .gcc	633

<210> 325

<211> 648

<212> DNA

<213> Homo sapiens

<400> 325

gatatcgac tgacccagcc agcttcagtg agcggctcac caggtcagag cattaccatc	60
tcgtgtacgg gtactagcag cgatgtggc ggctataact atgtgagctg gtaccagcag	120
catcccgaaa aggcgccgaa actgatgatt tatgatgtga gcaaccgtcc ctcaggcggt	180
agcaaccgtt ttagcggatc caaaagcggc aacaccgca gcctgaccat tagcggctg	240
caagcggaaag acgaagcggta ttattattgc cagagctatg acatgattgc tcgttatcct	300
gtgtttggcg gcggcacgaa gttaaccgtt cttggccagc cgaagccgc accgagtgtg	360
acgctgttc cggcgagcag cgaagaattt cagggcaaca aagcggccct ggtgtgcctg	420
attagcact tttatccggg agccgtgaca gtggcctgga aggccatag cagccccgtc	480
aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc	540
agctatctga gcctgacgccc tgagcagtgg aagtcccaca gaagctacag ctgccaggc	600
acgcattgagg ggagcaccgt gggaaaaacc gttgcggcga ctgaggcc	648

<210> 326

<211> 639

<212> DNA

<213> Homo sapiens

<400> 326

gatatcgaaac tgacccagcc gccttcagtg agcgttgac caggtcagac cgcgcgtatc	60
tcgtgtagcg gcgtgcgtc gggcgataaa tacgcgagct ggtaccagca gaaaccggg	120
caggcgccag tttctggat ttatgatgtat tctgaccgtc cctcaggcat cccggaaacgc	180
tttagcggat ccaacagcgg caacaccgcg accctgacca ttacggcgc tcaggcggaa	240
gacaagcgg attattattt ccagagctgg gacattcatc cttttgatgt tttgtttggc	300
ggccgcacgaa agttaaccgt tcttggccag ccgaaagccg caccgagtgt gacgctgttt	360
ccggcgagca gcaagaattt gcaggcgaac aaagcggaccc ttgtgtgcct gattagcgc	420
ttttatccgg gaggccgtac agtggcctgg aaggccatag gcagccccgt caaggcgggaa	480
gtggagacca ccacaccctc caaacaacaaac aacaacaatg acggccgcag cagctatctg	540
agctgtacgc ctgagcagtg gaagtcccac agaagctaca gctgccaggta cacgcacatg	600
gggagcaccg tggaaaaaac cgttgcggc actgaggcc	639

<210> 327

<211> 639

<212> DNA

<213> Homo sapiens

<400> 327

gatatcgatc tgacccagcc gccttcagtg agtggcgcac caggtcagcg tgtgaccatc	60
tcgtgtagcg gcagcagcag caacattggc agcaactatg tgagctggta ccagcagttg	120

ccggggacgg	cgccgaaact	gctgatttat	gataacaacc	agcgccctc	aggcgtgccc	180
gatcgttta	gcggatccaa	aagcggcacc	agcgcgaccc	ttgcgattac	gggcctgcaa	240
agcaagacg	aagcggatta	ttattgcccag	agctgggacc	ttgagcctta	tgtgtttggc	300
ggccgcacga	agttaacccgt	tctggccag	ccgaaagccg	caccgagtgt	gacgctgtt	360
ccggcagaca	gcgaagaatt	gcagggcgaac	aaagcgaccc	tggtgtgccc	gattagcga	420
tttatccgg	gagccgtgac	agtggcctgg	aaggcagata	gcagccccgt	caaggcggga	480
gtggagacca	ccacaccctc	caaacaaaagc	aacaacaagt	acgcggccag	cagctatctg	540
agcctgacgc	ctgagcagtg	gaagtcccac	agaagctaca	gctgccaggt	cacgcattgag	600
gggagcaccg	tggaaaaaac	cgttgcgccc	actgaggcc			639

<210> 328

<211> 645

<212> DNA

<213> Homo sapiens

<400> 328

gatatcgac	tgacccagcc	agttcagtg	agcggctcac	caggtcagag	cattaccatc	60
tcgtgtacgg	gtactagcag	cgatgtggc	ggctataact	atgtgagctg	gtaccagcag	120
catcccgga	aggcgccaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
agcaaccgtt	ttagcgatc	caaagcggc	aacaccgcga	gcctgaccat	tagccgcctg	240
caagcggaaag	acgaagcgg	ttattattgc	cagagctatg	acgttcttga	ttctgaggtg	300
tttggcggcg	gcacgaagtt	aaccgttctt	ggccagccga	aagccgcacc	gagtgtgacg	360
ctgtttccgc	cgagcagcga	agaattgcag	gcaacaaag	cgaccctgg	gtgcctgatt	420
agcactttt	atccgggagc	cgtgacagtg	gcctggaagg	cagatagcag	ccccgtcaag	480
gcgggagtgg	agaccaccac	accctccaaa	caaagcaaca	acaagtacgc	ggccagcagc	540
tatctgagcc	tgacgcctga	gcagtggaa	tcccacagaa	gctacagctg	ccaggtcaccg	600
catgagggga	gcaccgtgga	aaaaaccgtt	gcccgcactg	aggcc		645

<210> 329

<211> 648

<212> DNA

<213> Homo sapiens

<400> 329

gatatcgac	tgacccagcc	agttcagtg	agcggctcac	caggtcagag	cattaccatc	60
tcgtgtacgg	gtactagcag	cgatgtggc	ggctataact	atgtgagctg	gtaccagcag	120
catcccgga	aggcgccaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
agcaaccgtt	ttagcgatc	caaagcggc	aacaccgcga	gcctgaccat	tagccgcctg	240
caagcggaaag	acgaagcgg	ttattattgc	cagagctatg	acccttctca	tccttctaa	300
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acgcttcc	cgccgcacgc	cgaagaattg	caggcgaaca	aagcaccct	ggtgtgcctg	420
attagcgact	tttatccggg	agccgtgaca	gtggcctgga	aggcagatag	cagccccgtc	480
aaggcgggag	tggagaccac	cacaccctcc	aaacaaaagc	acaacaagt	cgccggccagc	540
agctatctga	gcctgacgccc	tgagcagtgg	aaagtcccaca	gaagctacag	ctgcccaggc	600
acgcatgagg	ggagcaccgt	ggaaaaacc	gttgcgccc	ctgaggcc		648

<210> 330

<211> 642

<212> DNA

<213> Homo sapiens

<400> 330

gatatcgac	tgacccagcc	agttcagtg	agcggctcac	caggtcagag	cattaccatc	60
tcgtgtacgg	gtactagcag	cgatgtggc	ggctataact	atgtgagctg	gtaccagcag	120
catcccgaa	aggcgccaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
agcaaccgtt	ttagcgatc	caaaagcgcc	aacaccgcga	gcctgaccat	tagcggctg	240
caagcggaa	acgaagcgga	ttattattgc	cagagctatg	acgatatgca	gtttgtt	300
ggccggcga	cgaagttaac	cgttcttggc	cagccgaaag	ccgcaccgag	tgtgacgctg	360
tttccggca	gcagcgaaga	attgcaggcg	aacaaagcg	ccctgggtgt	cctgattagc	420
gactttatc	cgggagccgt	gacagtggcc	ttgaaggcag	atagcagccc	cgtcaaggcg	480
ggagtggaga	ccaccacacc	ctccaaacaa	agcaacaaca	agtacgcggc	cagcagctat	540
ctgagcctga	cgcctgagca	gtgaaagtcc	cacagaagct	acagctgcca	ggtcacgcac	600
gaggggagca	ccgtggaaaa	aaccgttgcg	ccgactgagg	cc		642

<210> 331

<211> 645

<212> DNA

<213> Homo sapiens

<400> 331

gatatcgac	tgacccagcc	agttcagtg	agcggctcac	caggtcagag	cattaccatc	60
tcgtgtacgg	gtactagcag	cgatgtggc	ggctataact	atgtgagctg	gtaccagcag	120
catcccgaa	aggcgccaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
agcaaccgtt	ttagcgatc	caaaagcgcc	aacaccgcga	gcctgaccat	tagcggctg	240
caagcggaa	acgaagcgga	ttattattgc	cagagctgg	acattaatca	tgctatttg	300
tttggcggcg	gcacgaagtt	aaccgttctt	ggccagccga	aagccgcacc	gagtgtgacg	360
ctgtttccgc	cgagcagcg	agaattgcag	gcaacaaag	cgaccctgg	gtgcctgatt	420
agcactttt	atccgggagc	cgtgacagtg	gcctggaaagg	cagatagcag	ccccgtcaag	480
gcgggagtgg	agaccaccac	accctccaaa	caaagcaaca	acaagtacgc	ggccagcagc	540
tatctgagcc	tgacgcctga	gcagtggaa	tcccacagaa	gctacagctg	ccaggtcacg	600
cataggggaa	gcaccgtgga	aaaaaccgtt	gcccgcactg	aggcc		645

<210> 332

<211> 645

<212> DNA

<213> Homo sapiens

<400> 332

gatatcgac	tgacccagcc	agttcagtg	agcggctcac	caggtcagag	cattaccatc	60
tcgtgtacgg	gtactagcag	cgatgtggc	ggctataact	atgtgagctg	gtaccagcag	120
catcccgaa	aggcgccaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
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ctgtttccgc	cgagcagcg	agaattgcag	gcaacaaag	cgaccctgg	gtgcctgatt	420
agcactttt	atccgggagc	cgtgacagtg	gcctggaaagg	cagatagcag	ccccgtcaag	480
gcgggagtgg	agaccaccac	accctccaaa	caaagcaaca	acaagtacgc	ggccagcagc	540
tatctgagcc	tgacgcctga	gcagtggaa	tcccacagaa	gctacagctg	ccaggtcacg	600
cataggggaa	gcaccgtgga	aaaaaccgtt	gcccgcactg	aggcc		645

<210> 333
 <211> 645
 <212> DNA
 <213> Homo sapiens

<400> 333

gatatcggtgc	tgacccagag	cccgccgacc	ctgagcctgt	ctccggcgaa	acgtgcgacc	60
ctgagctgca	gagcgagcca	gagcgtgagc	agcagctatc	tggcgtggta	ccagcagaaa	120
ccaggtaag	caccgcgtct	attaattttat	ggcgcgagca	gccgtgcaac	tggggtccc	180
gcgcgtttta	gcggctctgg	atccggcacg	gattttaccc	tgaccattag	cagcctggaa	240
cctgaagact	ttgcggttta	ttatttgcag	caggctaatg	attttccat	taccttttggc	300
cagggtacga	aaagttgaaat	taaacgtacg	gtggctgctc	cgagcgtgtt	tatttttccg	360
ccgagcgtat	aacaactgaa	aagcggcacg	gcfagcgtgg	tgtgcctgct	gaacaacttt	420
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cagggaaagcg	tgaccgaaca	ggatagcaaa	gatagcacct	attctctgag	cagcaccctg	540
accctgagca	aagcggattt	tgaaaaacat	aaagtgtatg	cgtgcgaagt	gaccatcaa	600
ggtctgagca	gccccgggtgac	taaatctttt	aatcgtgcg	aggcc		645

<210> 334
 <211> 648
 <212> DNA
 <213> Homo sapiens

<400> 334

gatatcgcac	tgacccagcc	agcttcagtg	agcggctcac	caggtcagag	cattaccatc	60
tcgtgtacgg	gtactagcag	cgatgtgggc	ggctataact	atgtgagctg	gtaccagcag	120
catcccgaaa	aggcgccgaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
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caagcggaaag	acgaagcgg	ttattattgc	cagagctggg	acaatcttaa	gatgccttt	300
gtgtttggcg	gcggcacgaa	gttaaccgtt	cttggccagc	cgaagccgc	accgagtgt	360
acgctgtttc	cgccgagcag	cgaagaattt	caggcgaaca	aagcaccct	ggtgtgcctg	420
attagcgact	tttatccggg	agccgtgaca	gtggcctgga	aggcagatag	cagccccgtc	480
aaggcggggag	tggagaccac	cacaccctcc	aaacaagca	acaacaagta	cgcggccagc	540
agctatctga	gcctgacgccc	tgagcagtgg	aagtcccaca	gaagctacag	ctgccagg	600
acgcatgagg	ggagcaccgt	ggaaaaaacc	gttgcggcga	ctgaggcc		648

<210> 335
 <211> 648
 <212> DNA
 <213> Homo sapiens

<400> 335

gatatcgcac	tgacccagcc	agcttcagtg	agcggctcac	caggtcagag	cattaccatc	60
tcgtgtacgg	gtactagcag	cgatgtgggc	ggctataact	atgtgagctg	gtaccagcag	120
catcccgaaa	aggcgccgaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
agcaaccgtt	ttagcggatc	caaaagcggc	aacaccgcga	gcctgaccat	tagcggcctg	240
caagcggaaag	acgaagcgg	ttattattgc	cagagctatg	acgtttttcc	tattaatcgt	300
gtgtttggcg	gcggcacgaa	gttaaccgtt	cttggccagc	cgaagccgc	accgagtgt	360
acgctgtttc	cgccgagcag	cgaagaattt	caggcgaaca	aagcaccct	ggtgtgcctg	420
attagcgact	tttatccggg	agccgtgaca	gtggcctgga	aggcagatag	cagccccgtc	480

aaggcgggag tggagaccac cacaccctcc aaacaaagca acaacaagta cgcggccagc	540
acttatctga gcctgacgcc tgagcagtgg aagtcccaca gaagctacag ctgccaggc	600
acgcatgagg ggagcaccgt gaaaaaaacc gttgcgccga ctgaggcc	648

<210> 336

<211> 639

<212> DNA

<213> Homo sapiens

<400> 336

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tcgtgtacgg gtactagcag cgatgtggc ggctataact atgtgagctg gtaccagcag	120
catcccgaa aggcgcccactgatgatt tatgatgtga gcaaccgtcc ctcaggcgtg	180
agcaaccgtt ttagcggatc caaaaagcggc aacaccgcga gcctgaccat tagcggcctg	240
caagcggaa agcgaagcggat tattattgc cagagcgtatc ttatattcc tttgtttggc	300
ggcggcacgaa agttaaccgt tcttggccag cccgaaagccg caccgagtgt gacgctgtt	360
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ttttatccgg gagccgtgac agtggctgg aaggcagata gcagccccgt caaggcgggaa	480
gtggagacca ccacaccctc caaacaaaagc aacaacaagt acggggccag cagctatctg	540
agctgtacgc ctgagcgtg gaagtcccac agaagctaca gctgccaggt cacgcgtatgag	600
gggagcaccg tggaaaaaac cgttgcgcgg actgaggcc	639

<210> 337

<211> 642

<212> DNA

<213> Homo sapiens

<400> 337

gatatcgac tgacccagcc agttcagtg agcggctcac caggtcagag cattaccatc	60
tcgtgtacgg gtactagcag cgatgtggc ggctataact atgtgagctg gtaccagcag	120
catcccgaa aggcgcccactgatgatt tatgatgtga gcaaccgtcc ctcaggcgtg	180
agcaaccgtt ttagcggatc caaaaagcggc aacaccgcga gcctgaccat tagcggcctg	240
caagcggaa agcgaagcggat tattattgc cagagctatc acgttactcc tcgtgtgtt	300
ggcggccgca cgaagttaac cgttcttggc cagccgaaag ccgcaccgag tttgtgacgctg	360
tttccggcga gcagcgaaga attgcaggcg aacaaagcga ccctgggtgtg cctgattagc	420
gactttatc cgggagccgt gacagtggcc tggaggcag atagcagccc cgtcaaggcg	480
ggagtggaga ccaccacacc ctccaaacaa agcaacaaca agtacgcggc cagcagctat	540
ctgagcctga cgcctgagca gtggaaagtcc cacagaagct acagctgcca ggtcacgc	600
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<210> 338

<211> 636

<212> DNA

<213> Homo sapiens

<400> 338

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tcgtgtacgg gcgatgcgt gggcgataaa tacgcgagct ggtaccagca gaaacccggg	120
caggcggccat ttctggat tatgatgtatc tctgaccgtc cctcaggcat cccggaaacgc	180
tttagcggat ccaacagcgg caacaccgcg accctgacca ttagcggcac tcaggcggaa	240

gacgaagcgg	attattattg	ccagagccgt	gaccctgttgc	gtttcctgt	gtttggcggc	300
ggcacgaagt	taacogttct	tggccagccg	aaagccgcac	cgagtgtgac	gctgtttccg	360
ccgagcagcg	aagaatttgc	ggcgaacaaa	gcgaccctgg	tgtgcctgat	tagcactt	420
tatccgggag	ccgtgacagt	ggccttggaa	gcagatagca	gccccgtcaa	ggcgggagtg	480
gagaccacca	caccctccaa	acaaggcaac	aacaagtacg	cgccagcag	ctatctgagc	540
ctgacgcctg	agcagtgaa	gtcccacaga	agctacagct	gccaggtcac	gcatgagggg	600
agcaccgtgg	aaaaaaccgt	tgcgccact	gaggcc			636

<210> 339

<211> 642

<212> DNA

<213> Homo sapiens

<400> 339

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catccccggg	aggcgccgaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
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caagcggaaag	acgaagcgg	ttattattgc	cagagctatg	acctttctcc	tcgtgtgtt	300
ggccggcggca	cgaagttaac	cgttcttggc	cagccgaaag	ccgcaccgag	tgtgacgctg	360
tttccggcga	gcagcgaaga	attgcaggcg	aacaaagcga	cccttgggtg	cctgattagc	420
gacttttac	cgggagccgt	gacagtggcc	tggaaaggcag	atagcagccc	cgtcaaggcg	480
ggagtggaga	ccaccacacc	ctccaaacaa	agcaacaaca	agtacgcggc	cagcagctat	540
ctgagcctga	cgcctgagca	gtggaaagtcc	cacagaagct	acagtcgcca	ggtcacgcat	600
gaggggagca	ccgtggaaaa	aaccgttgcg	ccgactgagg	cc		642

<210> 340

<211> 648

<212> DNA

<213> Homo sapiens

<400> 340

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tcgtgtacgg	gtactagcag	cgatgtggc	ggctataact	atgtgagctg	gtaccagcag	120
catccccggg	aggcgccgaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
agcaaccgtt	ttagcgatc	caaaagcggc	aacaccgcga	gcctgaccat	tagcggcctg	240
caagcggaaag	acgaagcgg	ttattattgc	cagagctatg	actttctca	ttatttttt	300
gtgtttggcg	gcggcacgaa	gttaaccgtt	cttggccagc	cgaagccgc	accgagtgt	360
acgctgtttc	cgccgaggag	cgaagaattt	caggcgaaca	aagcaccct	gttgtgcctg	420
attagcgact	tttatccggg	agccgtgaca	gtggcctgga	aggcagatag	cagccccgtc	480
aaggcggggag	tggagaccac	cacaccctcc	aaacaaagca	acaacaagta	cgcggccagc	540
agctatctga	gcctgacgccc	tgagcagtgg	aagtcccaca	gaagctacag	ctgccaggtc	600
acgcatgagg	ggagcaccgt	ggaaaaaacc	gttgcgcccga	ctgaggcc		648

<210> 341

<211> 636

<212> DNA

<213> Homo sapiens

<400> 341

gatatcgAAC	tgacCCAGCC	gcTTcAGTG	agcGTTGcAC	caggTCAGAC	cgCGCGTATC	60
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caggCGCCAG	ttCTGGTGT	ttATGATGAT	tctGACCCTC	cCTCAGGCA	cccGGAAACGC	180
tttagCGGAT	ccaACAGCGG	caACACCGCG	accCTGACCA	ttAGCGGCAC	tcAGGCGGAA	240
gacaAGCGG	attATTATTG	ccAGAGCTAT	gacTTCTGTT	attCTCATGT	tttGGCGGC	300
ggcacGAAGT	taACCCTCT	tggCCAGCCG	aaAGCCGCAC	cgAGTGTGAC	gCTGTTCCG	360
ccgAGCAGCG	aagaATTGCA	ggCGAACAAA	gCGACCCTGG	tGTGCCTGAT	tagCAGCTT	420
tatCCGGGAG	ccGTGACAGT	ggCCTGGAAG	gCAGATAGCA	gCCCCGTCAA	ggCGGGAGTG	480
gagACCACCA	caccCTCCAA	acAAAGCAAC	aacaAGTACG	cgGCCAGCAG	ctATCTGAGC	540
ctgacGCCTG	agCAGTGGAA	gtCCACAGA	agCTACAGCT	gCCAGGTAC	gCATGAGGGG	600
agcaccGTGG	aaaaaACCGT	tgcGCCACT	gaggCC			636

<210> 342

<211> 642

<212> DNA

<213> Homo sapiens

<400> 342

gatatcgCAC	tgacCCAGCC	agTTcAGTG	agcGGCTCAC	caggTCAGAG	cattACCATC	60
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catCCCGGGA	aggCGCCGAA	actGATGATT	tatGATGTGA	gcaACCGTCC	ctcAGGCCTG	180
agcaACCGTT	ttAGCGGATC	caaAAAGCGGC	aaCACCGCGA	gcCTGACCAT	tagCGGCCTG	240
caagCGGAAG	acGAAGCGGA	ttATTATTGC	cAGAGCTATG	acCTTCTGAA	tCGTGTGTT	300
ggCGGCGGCA	cgaAGTTAAC	cgtTCTTGGC	cAGCGAAAG	ccgcACCGAG	tGTGACGCTG	360
tttCCGCCGA	gcAGCGAAGA	attGCGAGCG	aacaAGCGA	ccCTGGTGTG	cCTGATTAGC	420
gactTTATC	cggGAGCCGT	gacAGTGGCC	tggAAGGAG	atAGCAGCCC	cgtCAAGGCG	480
ggAGTGGAGA	ccACCACACC	ctCCAAACAA	agCAACAAACA	agtACGCGGC	cAGCAGCTAT	540
ctgacGCCTG	cgcCTGAGCA	gtGGAAGTCC	cACAGAAGCT	acAGTGCAC	ggtCACGCA	600
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<210> 343

<211> 645

<212> DNA

<213> Homo sapiens

<400> 343

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tcgtGTACGG	gtactAGCAG	cgATGTGGC	ggCTATAACT	atGTGAGCTG	gtaccAGCAG	120
catCCCGGGA	aggCGCCGAA	actGATGATT	tatGATGTGA	gcaACCGTCC	ctcAGGCCTG	180
agcaACCGTT	ttAGCGGATC	caaAAAGCGGC	aaCACCGCGA	gcCTGACCAT	tagCGGCCTG	240
caagCGGAAG	acGAAGCGGA	ttATTATTGC	cAGAGCTATG	acTTTACTTA	tGTTTCTGTG	300
tttGGCGCG	gcACGAAGTT	aaccGTTCTT	ggCCAGCCGA	aAGCCGCACC	gagtGTGACG	360
ctGTTTCCGC	cgAGCAGCGA	agaATTGCA	gCGAACAAAG	cgACCCCTGGT	gtGCCTGATT	420
agcACTTT	atCCGGGAGC	cgtGACAGTG	gcCTGGAAGG	cAGATAGCAG	ccccGTCAAG	480
gcGGGAGTGG	agACCACAC	accCTCCAAA	caaAGCAACA	acaAGTACG	ggCCAGCAGC	540
tatCTGAGCC	tgacGCCTG	gCAGTGGAA	tcccACAGAA	gCTACAGCTG	ccAGGTAC	600
catGAGGGGA	gcaccGTGGA	aaaaaACCGT	gCGCCGACTG	aggCC		645

<210> 344

<211> 645

<212> DNA

<213> Homo sapiens

<400> 344

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ccaggtcaag	caccgcgtct	attaatttat	ggcgcgagca	gccgtgcaac	tggggtcccg	180
gcgcgttta	gcggctctgg	atccggcacg	gattttaccc	tgaccattag	cagcctggaa	240
cctgaagact	ttgcggttta	ttattgcccag	cagtttaatg	atttcctta	tacctttggc	300
cagggtacga	aagttgaat	taaacgtacg	gtggctgctc	cgagcgtgtt	tattttccg	360
ccgagcgatg	aacaactgaa	aaggcgacg	gcgagcgtgg	tgtgcctgct	gaacaacttt	420
tatccgcgtg	aagcgaaagt	tcagtggaaa	gtagacaacg	cgctgcaaag	cggcaacagc	480
cagggaaagcg	tgaccgaaca	ggatagcaaa	gatagcacct	attctctgag	cagcaccctg	540
accctgagca	aaggcgattt	tgaaaaacat	aaagtgtatg	cgtgcgaagt	gaccatcaa	600
ggctcgagca	gcccggtgac	taaatcttt	aatcggtggc	aggcc		645

<210> 345

<211> 649

<212> DNA

<213> Homo sapiens

<400> 345

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gcagcatccc	gggaaggcg	cgaaactgtat	gatttatgtat	gtgagcaacc	gtccctcagg	180
cgtgagcaac	cgtttttagcg	gatccaaaag	cggaacacacc	gcgagcctga	ccattagcg	240
cctgcaagcg	gaagacgaag	cggttattat	ttgcccagac	tatgacattt	ctggttatcc	300
tgtgtttggc	ggcggcacg	agtttaccgt	tcttggccag	ccgaaagccg	caccgagtgt	360
gacgctgttt	ccggcgagca	gcgaagaatt	gcaggcgaac	aaagcgaccc	tggtgtgcct	420
gattagcgac	ttttatccgg	gagccgtgac	agtggcctgg	aaggcagata	gcagccccgt	480
caaggcgaaa	gtggagacca	ccacaccctc	caaacaaga	aacaacaagt	acgcggccag	540
cagctatctg	agcctgacgc	ctgagcgttg	gaagtccac	agaagctaca	gctgccaggt	600
cacgcattag	gggagcaccg	tggaaaaaac	cgttgcggc	actgaggcc		649

<210> 346

<211> 648

<212> DNA

<213> Homo sapiens

<400> 346

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catcccgaaa	aggcgccgaa	actgtatgt	tatgtatgt	gcaaccgtcc	ctcaggcg	180
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caagcgaaag	acgaaggcga	ttattattgc	cagagccgt	acctttatata	tgtttattat	300
gtgtttggc	gcggcacaa	gttaaccgtt	cttggccagc	cgaagccgc	accgagtgt	360
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aaggcgaaa	tggagaccac	cacaccctc	aaacaaga	acaacaagta	cgccggccagc	540
agctatctg	gcctgacg	ctgagcgttg	aaagtccac	gaagctacag	ctgccaggtc	600

acgcatgagg ggagcaccgt ggaaaaaacc gttgcgccga ctgaggcc	648
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<211> 633	
<212> DNA	
<213> Homo sapiens	
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acgaagttaa ccgttcttgg ccagccgaaa gccgcaccga gtgtgacgtc gtttccggcg	360
agcagcgaag aattgcaggc gaacaaagcg accctgggtgt gcctgatttag cgacttttat	420
ccgggagccg tgacagtggc ctggaggca gatagcagcc ccgtcaaggc gggagtgagg	480
accaccacac cctccaaaca aagcaacaac aagtacgcgg ccagcagcta tctgagcctg	540
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<210> 348	
<211> 645	
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catcccgaaa aggcgcccggaa actgatgatt tatgtatgtat gcaaccgtcc ctcaggcgat	180
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gagaccacca caccctccaa acaaagcaac aacaagtacg cggccagcag ctatctgagc	540
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<210> 350

<211> 645

<212> DNA

<213> Homo sapiens

<400> 350

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<400> 351

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<210> 352

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<400> 352

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<210> 353

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<400> 353

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catcccggga	aggcgccgaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
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catcccggga	aggcgccgaa	actgatgatt	tatgatgtga	gcaaccgtcc	ctcaggcgtg	180
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caagcggaaag	acgaagcggc	ttattattgc	cagagcgtaca	atccttatct	tgtgtttggc	300
ggccgcacga	agttAACCGT	tcttggccag	ccgaaagccg	caccgagtgt	gacgctgttt	360
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<213> Homo sapiens

<400> 355
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1 5 10

<210> 356
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1 5 10

<210> 357
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<400> 357
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1 5 10 15
Gly

<210> 358
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